

# Sequence Listing

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 Baker Kevin P.  
 Botstein, David  
 Desnoyers, Luc  
 Eaton, Dan  
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 Fong, Sherman  
 Gao, Wei-Qiang  
 Gerber, Hanspeter  
 Gerritsen, Mary E.  
 Goddard, Audrey  
 Godowski, Paul J.  
 Grimaldi, J. Christopher  
 Gurney, Austin L.  
 Hillan, Kenneth J.  
 Kljavin, Ivar J.  
 Kuo, Sophia S.  
 Napier, Mary A.  
 Pan, James;  
 Paoni, Nicholas F.  
 Roy, Margaret Ann  
 Shelton, David L.  
 Stewart, Timothy A.  
 Tumas, Daniel  
 Williams, P. Mickey  
 Wood, William I.

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aggtcgagag aaggccatgg aggtgccgcc accggcaccg cggagctttc 200  
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Sequence 430004

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 ttaatctatc aatatatgca tacatggata tatccacca cctagatttt 1300  
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t 1351

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<211> 285

<212> PRT

<213> Homo sapiens

<400> 28

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Leu	Cys	Leu	Phe	Pro	Arg	Val	Phe	Ala	Ala	Glu	Ala	Val	Thr	Ala
				20				25					30	





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 tgaacagcag agaatttcaa aggaccttgc taatatctgt aagacggcag 150  
 ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt 200  
 catgctaaac aacaatacat tgagcagagc caggcagaaa tttatcataa 250  
 ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca cgaggcttca 300  
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<210> 30  
 <211> 377  
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 <221> unsure  
 <222> 262, 330, 371  
 <223> unknown base

FOOT-HSOUT-FOOT

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 gctgccgaag ctgtgactgc cgattcggaa gtccttgagg agcgtcagaa 150  
 gcggcttccc tacgtccag agccctatta cccggaattt ggatgggacc 200  
 gcctccggga gctgtttggc aaagatgaac agcagagaat ttcaaaggac 250  
 cttgtgata tntgtaagac ggcagctaca gcaggcatca ttggctgggt 300  
 gtatggggga ataccagctt ttattcatgn taaacaacaa tacattgagc 350  
 agagccaggc agaaatttat nataacc 377

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<220>  
 <223> Synthetic oligonucleotide probe

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<210> 32  
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<220>  
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<400> 32  
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<210> 33  
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ataacgaatg aagcctcgtg 20

<210> 34  
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<210> 35  
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protein database

Ala Ala Trp Gly Ile Gly Phe Gly Leu Ile Ser Ser Leu Arg Val  
35 40 45  
Val Gly Val Val Ile Ala Val Gly Ile Phe Leu Phe Leu Ile Ala  
50 55 60  
Leu Val Gly Leu Ile Gly Ala Val Lys His His Gln Val Leu Leu  
65 70 75  
Phe Phe Tyr Met Ile Ile Leu Leu Leu Val Phe Ile Val Gln Phe  
80 85 90  
Ser Val Ser Cys Ala Cys Leu Ala Leu Asn Gln Glu Gln Gln Gly  
95 100 105  
Gln Leu Leu Glu Val Gly Trp Asn Asn Thr Ala Ser Ala Arg Asn  
110 115 120  
Asp Ile Gln Arg Asn Leu Asn Cys Cys Gly Phe Arg Ser Val Asn  
125 130 135  
Pro Asn Asp Thr Cys Leu Ala Ser Cys Val Lys Ser Asp His Ser  
140 145 150  
Cys Ser Pro Cys Ala Pro Ile Ile Gly Glu Tyr Ala Gly Glu Val  
155 160 165  
Leu Arg Phe Val Gly Gly Ile Gly Leu Phe Phe Ser Phe Thr Glu  
170 175 180  
Ile Leu Gly Val Trp Leu Thr Tyr Arg Tyr Arg Asn Gln Lys Asp  
185 190 195  
Pro Arg Ala Asn Pro Ser Ala Phe Leu  
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<210> 37  
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<221> unsure  
<222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336  
<223> unknown base

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<210> 38  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 27  
 <223> unknown base

<400> 38  
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 ttacaccaat gtattctaga atagtattgt cttaggaaat tgtggtttaa 150  
 tttttgactt ttacaggtaa gtgcaaagga gaagtggttt catgaaatgt 200  
 tctaattgtat aataacattt accttcagcc tcccatcaga atggaaccag 250  
 ttttgagtaa tccaggaagt atatctatat gatcttgata ttgttttata 300  
 taatttgaag tctaaaagac tgcattttta aacaagttag tattaatgcg 350  
 ttggcccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaaata 400  
 ccgttttcat gaaagtctc agtattgtaa cagcaacttg tcaaacctaa 450  
 gcatatttga atatgatctc ccataatttg aaattgaaat cgtattgtgt 500  
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 gttgtgcccc acttgc 566

<210> 39  
 <211> 264  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 84-85, 206  
 <223> unknown base

<400> 39  
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 aatcctaaac tgctgtgggt tccgaagtgt taaccctaat gacacctgtc 200

FOH201-1304-1001

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ataggagaat atgc 264

<210> 40

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 40

accacgtct gcgttgctgc c 21

<210> 41

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 41

gagaatatgc tggagagg 18

<210> 42

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 42

aggaatgcac taggattcgc gcgg 24

<210> 43

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 43

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<210> 44

<211> 2061

<212> DNA

<213> Homo sapiens

<400> 44

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<220>  
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<400> 47  
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<210> 48  
<211> 23  
<212> DNA  
<213> Artificial Sequence

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<210> 49  
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<212> DNA  
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<220>  
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<210> 51  
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<213> Homo sapiens

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<210> 52

<211> 321

<212> PRT

<213> Homo sapiens

<400> 52

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Gly	Pro	Trp	Lys	Gly	Asp	Val	Asn	Leu	Pro	Cys	Thr	Tyr	Asp	Pro	35	40	45	
Leu	Gln	Gly	Tyr	Thr	Gln	Val	Leu	Val	Lys	Trp	Leu	Val	Gln	Arg	50	55	60	
Gly	Ser	Asp	Pro	Val	Thr	Ile	Phe	Leu	Arg	Asp	Ser	Ser	Gly	Asp	65	70	75	
His	Ile	Gln	Gln	Ala	Lys	Tyr	Gln	Gly	Arg	Leu	His	Val	Ser	His	80	85	90	
Lys	Val	Pro	Gly	Asp	Val	Ser	Leu	Gln	Leu	Ser	Thr	Leu	Glu	Met	95	100	105	
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Gln	Lys	Leu	Ser	Val	Ser	Lys	Pro	Thr	Val	Thr	Thr	Gly	Ser	Gly	140	145	150	
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Gln	Ala	Arg	Gly	Ser	Pro	Pro	Ile	Ser	Tyr	Ile	Trp	Tyr	Lys	Gln	170	175	180	

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185 190 195

Leu Leu Phe Lys Pro Ala Val Ile Ala Asp Ser Gly Ser Tyr Phe  
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Cys Thr Ala Lys Gly Gln Val Gly Ser Glu Gln His Ser Asp Ile  
215 220 225

Val Lys Phe Val Val Lys Asp Ser Ser Lys Leu Leu Lys Thr Lys  
230 235 240

Thr Glu Ala Pro Thr Thr Met Thr Tyr Pro Leu Lys Ala Thr Ser  
245 250 255

Thr Val Lys Gln Ser Trp Asp Trp Thr Thr Asp Met Asp Gly Tyr  
260 265 270

Leu Gly Glu Thr Ser Ala Gly Pro Gly Lys Ser Leu Pro Val Phe  
275 280 285

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290 295 300

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305 310 315

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<223> Synthetic oligonucleotide probe

<400> 53  
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<210> 54  
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<220>



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<210> 59

<211> 373

<212> PRT

<213> Homo sapiens

<400> 59

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20 25 30

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35 40 45

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Lys Val Val Ile Thr Tyr Ser Ser Arg His Val Tyr Asn Asn Leu  
65 70 75

Thr Glu Glu Gln Lys Gly Arg Val Ala Phe Ala Ser Asn Phe Leu  
80 85 90

Ala Gly Asp Ala Ser Leu Gln Ile Glu Pro Leu Lys Pro Ser Asp  
95 100 105

Glu Gly Arg Tyr Thr Cys Lys Val Lys Asn Ser Gly Arg Tyr Val  
110 115 120

Trp Ser His Val Ile Leu Lys Val Leu Val Arg Pro Ser Lys Pro  
125 130 135

Lys Cys Glu Leu Glu Gly Glu Leu Thr Glu Gly Ser Asp Leu Thr  
140 145 150

Leu Gln Cys Glu Ser Ser Ser Gly Thr Glu Pro Ile Val Tyr Tyr  
155 160 165

Trp Gln Arg Ile Arg Glu Lys Glu Gly Glu Asp Glu Arg Leu Pro  
170 175 180





<400> 61  
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<210> 62

<211> 43

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 63

<211> 3534

<212> DNA

<213> Homo sapiens

<400> 63

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 <211> 655  
 <212> PRT  
 <213> Homo sapiens

<400> 64  
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 20 25 30



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Pro Lys Arg Gly His	Pro Arg Gln Asn Leu His Lys His Phe Asp	
335	340	345
Ile Asn Glu His Leu	Pro Trp Met Ile Val Leu Phe Leu Leu Leu	
350	355	360
Val Leu Val Val Ile	Val Val Cys Ser Ile Arg Lys Ser Ser Arg	
365	370	375
Thr Leu Lys Lys Gly	Pro Arg Gln Asp Pro Ser Ala Ile Val Glu	
380	385	390
Lys Ala Gly Leu Lys	Lys Ser Met Thr Pro Thr Gln Asn Arg Glu	
395	400	405
Lys Trp Ile Tyr Tyr	Cys Asn Gly His Gly Ile Asp Ile Leu Lys	
410	415	420
Leu Val Ala Ala Gln	Val Gly Ser Gln Trp Lys Asp Ile Tyr Gln	
425	430	435
Phe Leu Cys Asn Ala	Ser Glu Arg Glu Val Ala Ala Phe Ser Asn	
440	445	450
Gly Tyr Thr Ala Asp	His Glu Arg Ala Tyr Ala Ala Leu Gln His	
455	460	465
Trp Thr Ile Arg Gly	Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser	
470	475	480
Ala Leu Arg Gln His	Arg Arg Asn Asp Val Val Glu Lys Ile Arg	
485	490	495
Gly Leu Met Glu Asp	Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala	
500	505	510
Leu Pro Met Ser Pro	Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser	
515	520	525
Pro Asn Ala Lys Leu	Glu Asn Ser Ala Leu Leu Thr Val Glu Pro	
530	535	540
Ser Pro Gln Asp Lys	Asn Lys Gly Phe Phe Val Asp Glu Ser Glu	
545	550	555
Pro Leu Leu Arg Cys	Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu	
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Ser Arg Asn Gly Ser	Phe Ile Thr Lys Glu Lys Lys Asp Thr Val	
575	580	585
Leu Arg Gln Val Arg	Leu Asp Pro Cys Asp Leu Gln Pro Ile Phe	
590	595	600
Asp Asp Met Leu His	Phe Leu Asn Pro Glu Glu Leu Arg Val Ile	
605	610	615

Glu Glu Ile Pro Gln Ala Glu Asp Lys Leu Asp Arg Leu Phe Glu  
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Ile Ile Gly Val Lys Ser Gln Glu Ala Ser Gln Thr Leu Leu Asp  
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Ser Val Tyr Ser His Leu Pro Asp Leu Leu  
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<211> 24  
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<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 65  
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<210> 66  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 66  
accgcacatc ctgagttctt gtcc 24

<210> 67  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
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<210> 68  
<211> 2412  
<212> DNA  
<213> Homo sapiens

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 <211> 453  
 <212> PRT  
 <213> Homo sapiens

<400> 69  
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 Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile  
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 Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly  
 65 70 75  
 Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala  
 80 85 90  
 Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr  
 95 100 105  
 Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe

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125	130	135
His Tyr Ala Asn Val Ala Cys Ala Gln	Leu Gly Phe Pro Ser Tyr	
140	145	150
Val Ser Ser Asp Asn Leu Arg Val Ser	Ser Leu Glu Gly Gln Phe	
155	160	165
Arg Glu Glu Phe Val Ser Ile Asp His	Leu Leu Pro Asp Asp Lys	
170	175	180
Val Thr Ala Leu His His Ser Val Tyr	Val Arg Glu Gly Cys Ala	
185	190	195
Ser Gly His Val Val Thr Leu Gln Cys	Thr Ala Cys Gly His Arg	
200	205	210
Arg Gly Tyr Ser Ser Arg Ile Val Gly	Gly Asn Met Ser Leu Leu	
215	220	225
Ser Gln Trp Pro Trp Gln Ala Ser Leu	Gln Phe Gln Gly Tyr His	
230	235	240
Leu Cys Gly Gly Ser Val Ile Thr Pro	Leu Trp Ile Ile Thr Ala	
245	250	255
Ala His Cys Val Tyr Asp Leu Tyr Leu	Pro Lys Ser Trp Thr Ile	
260	265	270
Gln Val Gly Leu Val Ser Leu Leu Asp	Asn Pro Ala Pro Ser His	
275	280	285
Leu Val Glu Lys Ile Val Tyr His Ser	Lys Tyr Lys Pro Lys Arg	
290	295	300
Leu Gly Asn Asp Ile Ala Leu Met Lys	Leu Ala Gly Pro Leu Thr	
305	310	315
Phe Asn Glu Met Ile Gln Pro Val Cys	Leu Pro Asn Ser Glu Glu	
320	325	330
Asn Phe Pro Asp Gly Lys Val Cys Trp	Thr Ser Gly Trp Gly Ala	
335	340	345
Thr Glu Asp Gly Gly Asp Ala Ser Pro	Val Leu Asn His Ala Ala	
350	355	360
Val Pro Leu Ile Ser Asn Lys Ile Cys	Asn His Arg Asp Val Tyr	
365	370	375
Gly Gly Ile Ile Ser Pro Ser Met Leu	Cys Ala Gly Tyr Leu Thr	
380	385	390
Gly Gly Val Asp Ser Cys Gln Gly Asp	Ser Gly Gly Pro Leu Val	
395	400	405

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Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe  
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Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg  
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 440 445 450

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<210> 70  
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 <212> DNA  
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<220>  
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<400> 70  
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<210> 71  
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 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 71  
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<210> 73  
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 <212> DNA  
 <213> Homo sapiens

<400> 73  
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 <211> 735  
 <212> PRT  
 <213> Homo sapiens

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 Ser Val Arg Ser Gly Asp Leu Trp Ile Pro Val Lys Ser Phe Asp  
 50 55 60  
 Ser Lys Asn His Pro Glu Val Leu Asn Ile Arg Leu Gln Arg Glu  
 65 70 75  
 Ser Lys Glu Leu Ile Ile Asn Leu Glu Arg Asn Glu Gly Leu Ile  
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 Ala Ser Ser Phe Thr Glu Thr His Tyr Leu Gln Asp Gly Thr Asp  
 95 100 105  
 Val Ser Leu Ala Arg Asn Tyr Thr Gly His Cys Tyr Tyr His Gly  
 110 115 120  
 His Val Arg Gly Tyr Ser Asp Ser Ala Val Ser Leu Ser Thr Cys  
 125 130 135  
 Ser Gly Leu Arg Gly Leu Ile Val Phe Glu Asn Glu Ser Tyr Val  
 140 145 150  
 Leu Glu Pro Met Lys Ser Ala Thr Asn Arg Tyr Lys Leu Phe Pro  
 155 160 165  
 Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys Gly Ser His His  
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 Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala Thr  
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230 235 240

Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn Ile Arg  
245 250 255

Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys Cys  
260 265 270

Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe Leu Asp  
275 280 285

Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn Ala  
290 295 300

Gln Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met  
305 310 315

Ala Pro Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile  
320 325 330

Val Met Asp His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu  
335 340 345

Ala His Glu Leu Gly His Asn Phe Gly Met Asn His Asp Thr Leu  
350 355 360

Asp Arg Gly Cys Ser Cys Gln Met Ala Val Glu Lys Gly Gly Cys  
365 370 375

Ile Met Asn Ala Ser Thr Gly Tyr Pro Phe Pro Met Val Phe Ser  
380 385 390

Ser Cys Ser Arg Lys Asp Leu Glu Thr Ser Leu Glu Lys Gly Met  
395 400 405

Gly Val Cys Leu Phe Asn Leu Pro Glu Val Arg Glu Ser Phe Gly  
410 415 420

Gly Gln Lys Cys Gly Asn Arg Phe Val Glu Glu Gly Glu Glu Cys  
425 430 435

Asp Cys Gly Glu Pro Glu Glu Cys Met Asn Arg Cys Cys Asn Ala  
440 445 450

Thr Thr Cys Thr Leu Lys Pro Asp Ala Val Cys Ala His Gly Leu  
455 460 465

Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala Gly Thr Ala Cys Arg  
470 475 480

Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe Cys Thr Gly Ala  
485 490 495

Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp Gly His Ser





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 gcagccctga taactggtnt ntggctgcaa nttaatgctn tgatatggct 400  
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<400> 77  
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<210> 78  
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 <223> Synthetic oligonucleotide probe

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<210> 79  
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TEORET-1302-1001

<220>  
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<400> 81  
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<210> 82  
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<223> Synthetic oligonucleotide probe

<400> 82  
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<212> DNA  
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<210> 84  
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<212> DNA  
<213> Homo sapiens

<400> 84  
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 aaccacaccc ggccacaaac tttttaagaa gttaatgaaa ccataccttt 200  
 tacattttta atgacaggaa aatgctcaca ataattgtta acccaaaatt 250  
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 gaatagcgtg aactcaggag gggagccttg cagtgcgagc agattgcgct 1650  
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 aaaaaaaaaa aaaa 1714

<210> 85  
 <211> 67  
 <212> PRT  
 <213> Homo sapiens

<400> 85  
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 20 25 30  
 Thr Ser Met Pro Glu Ala Thr Ala Ala Glu Thr Thr Lys Pro Ser  
 35 40 45  
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 50 55 60  
 Ala Leu Leu His Leu Tyr His  
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Feature = t60000

<210> 86  
 <211> 23  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 86  
 acgggcacac tggatcccaa atg 23

<210> 87  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 87  
 ggtagagatg tagaaggga agcaagacc 29

<210> 88  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 88  
gctccctacc cgtgcaggtt ttttcatttg ttcctttaac cagtatgccg 50

<210> 89  
<211> 2956  
<212> DNA  
<213> Homo sapiens

<400> 89  
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<210> 90  
 <211> 432  
 <212> PRT  
 <213> Homo sapiens

<400> 90  
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 35 40 45  
 Ala Asp Gly Pro Pro Ala Ala Asp Gly Glu Asp Gly Gln Asp Pro  
 50 55 60  
 His Ser Lys His Leu Tyr Thr Ala Asp Met Phe Thr His Gly Ile  
 65 70 75  
 Gln Ser Ala Ala His Phe Val Met Phe Phe Ala Pro Trp Cys Gly  
 80 85 90  
 His Cys Gln Arg Leu Gln Pro Thr Trp Asn Asp Leu Gly Asp Lys  
 95 100 105  
 Tyr Asn Ser Met Glu Asp Ala Lys Val Tyr Val Ala Lys Val Asp  
 110 115 120  
 Cys Thr Ala His Ser Asp Val Cys Ser Ala Gln Gly Val Arg Gly  
 125 130 135  
 Tyr Pro Thr Leu Lys Leu Phe Lys Pro Gly Gln Glu Ala Val Lys  
 140 145 150  
 Tyr Gln Gly Pro Arg Asp Phe Gln Thr Leu Glu Asn Trp Met Leu  
 155 160 165  
 Gln Thr Leu Asn Glu Glu Pro Val Thr Pro Glu Pro Glu Val Glu  
 170 175 180





<400> 91  
atgttcttcg cgccctggtg 20

<210> 92  
<211> 21  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 92  
ccaagccaac acactctaca g 21

<210> 93  
<211> 24  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 93  
aagtggtcgc cttgtgcaac gtgc 24

<210> 94  
<211> 23  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 94  
ggtcaaagg gatatatcgc cac 23

<210> 95  
<211> 49  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 95  
gcatggaaga tgccaaagtc tatgtggcta aagtggactg cacggcca 49

<210> 96  
<211> 1016  
<212> DNA  
<213> Homo sapiens

<400> 96  
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gtctggatat tgatagccgt cctaccgctg aagtctgtgc cacacacaca 150



80	85	90
Thr Gly Pro Ile Gly Lys Lys Gly Asp	Lys Gly Glu Lys Gly Leu	
95	100	105
Leu Gly Ile Pro Gly Glu Lys Gly Lys	Ala Gly Thr Val Cys Asp	
110	115	120
Cys Gly Arg Tyr Arg Lys Phe Val Gly	Gln Leu Asp Ile Ser Ile	
125	130	135
Ala Arg Leu Lys Thr Ser Met Lys Phe	Val Lys Asn Val Ile Ala	
140	145	150
Gly Ile Arg Glu Thr Glu Glu Lys Phe	Tyr Tyr Ile Val Gln Glu	
155	160	165
Glu Lys Asn Tyr Arg Glu Ser Leu Thr	His Cys Arg Ile Arg Gly	
170	175	180
Gly Met Leu Ala Met Pro Lys Asp Glu	Ala Ala Asn Thr Leu Ile	
185	190	195
Ala Asp Tyr Val Ala Lys Ser Gly Phe	Phe Arg Val Phe Ile Gly	
200	205	210
Val Asn Asp Leu Glu Arg Glu Gly Gln	Tyr Met Ser Thr Asp Asn	
215	220	225
Thr Pro Leu Gln Asn Tyr Ser Asn Trp	Asn Glu Gly Glu Pro Ser	
230	235	240
Asp Pro Tyr Gly His Glu Asp Cys Val	Glu Met Leu Ser Ser Gly	
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Arg Trp Asn Asp Thr Glu Cys His Leu	Thr Met Tyr Phe Val Cys	
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275		

130200T

<210> 98  
 <211> 24  
 <212> DNA  
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 <223> Synthetic oligonucleotide probe

<400> 98  
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<210> 99  
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 <212> DNA  
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<223> Synthetic oligonucleotide probe

<400> 99

gatgatggag gctccatacc tcag 24

<210> 100

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 100

gtgttcattg gcgtgaatga ccttgaaagg gagggacagt acatgttcac 50

<210> 101

<211> 2574

<212> DNA

<213> Homo sapiens

<400> 101

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<210> 102  
 <211> 730  
 <212> PRT  
 <213> Homo sapiens

<400> 102

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Met	Phe	Ala	Ser	Gly	Trp	Asn	Gln	Thr	Val	Pro	Ile	Glu	Glu	Ala	35	40	45	
Gly	Ser	Met	Ala	Ala	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	50	55	60	
Pro	Leu	Leu	Leu	Leu	Lys	Leu	His	Leu	Trp	Pro	Gln	Leu	Arg	Trp	65	70	75	
Leu	Pro	Ala	Asp	Leu	Ala	Phe	Ala	Val	Arg	Ala	Leu	Cys	Cys	Lys	80	85	90	
Arg	Ala	Leu	Arg	Ala	Arg	Ala	Leu	Ala	Ala	Ala	Ala	Asp	Pro	95	100	105		
Glu	Gly	Pro	Glu	Gly	Gly	Cys	Ser	Leu	Ala	Trp	Arg	Leu	Ala	Glu	110	115	120	
Leu	Ala	Gln	Gln	Arg	Ala	Ala	His	Thr	Phe	Leu	Ile	His	Gly	Ser	125	130	135	
Arg	Arg	Phe	Ser	Tyr	Ser	Glu	Ala	Glu	Arg	Glu	Ser	Asn	Arg	Ala	140	145	150	
Ala	Arg	Ala	Phe	Leu	Arg	Ala	Leu	Gly	Trp	Asp	Trp	Gly	Pro	Asp	155	160	165	
Gly	Gly	Asp	Ser	Gly	Glu	Gly	Ser	Ala	Gly	Glu	Gly	Glu	Arg	Ala	170	175	180	
Ala	Pro	Gly	Ala	Gly	Asp	Ala	Ala	Ala	Gly	Ser	Gly	Ala	Glu	Phe	185	190	195	
Ala	Gly	Gly	Asp	Gly	Ala	Ala	Arg	Gly	Gly	Gly	Ala	Ala	Ala	Pro	200	205	210	

Leu Ser Pro Gly	Ala Thr Val Ala Leu	Leu Leu Pro Ala Gly	Pro
215		220	225
Glu Phe Leu Trp	Leu Trp Phe Gly Leu	Ala Lys Ala Gly Leu	Arg
230		235	240
Thr Ala Phe Val	Pro Thr Ala Leu Arg	Arg Gly Pro Leu Leu	His
245		250	255
Cys Leu Arg Ser	Cys Gly Ala Arg Ala	Leu Val Leu Ala Pro	Glu
260		265	270
Phe Leu Glu Ser	Leu Glu Pro Asp Leu	Pro Ala Leu Arg Ala	Met
275		280	285
Gly Leu His Leu	Trp Ala Ala Gly Pro	Gly Thr His Pro Ala	Gly
290		295	300
Ile Ser Asp Leu	Leu Ala Glu Val Ser	Ala Glu Val Asp Gly	Pro
305		310	315
Val Pro Gly Tyr	Leu Ser Ser Pro Gln	Ser Ile Thr Asp Thr	Cys
320		325	330
Leu Tyr Ile Phe	Thr Ser Gly Thr Thr	Gly Leu Pro Lys Ala	Ala
335		340	345
Arg Ile Ser His	Leu Lys Ile Leu Gln	Cys Gln Gly Phe Tyr	Gln
350		355	360
Leu Cys Gly Val	His Gln Glu Asp Val	Ile Tyr Leu Ala Leu	Pro
365		370	375
Leu Tyr His Met	Ser Gly Ser Leu Leu	Gly Ile Val Gly Cys	Met
380		385	390
Gly Ile Gly Ala	Thr Val Val Leu Lys	Ser Lys Phe Ser Ala	Gly
395		400	405
Gln Phe Trp Glu	Asp Cys Gln Gln His	Arg Val Thr Val Phe	Gln
410		415	420
Tyr Ile Gly Glu	Leu Cys Arg Tyr Leu	Val Asn Gln Pro Pro	Ser
425		430	435
Lys Ala Glu Arg	Gly His Lys Val Arg	Leu Ala Val Gly Ser	Gly
440		445	450
Leu Arg Pro Asp	Thr Trp Glu Arg Phe	Val Arg Arg Phe Gly	Pro
455		460	465
Leu Gln Val Leu	Glu Thr Tyr Gly Leu	Thr Glu Gly Asn Val	Ala
470		475	480
Thr Ile Asn Tyr	Thr Gly Gln Arg Gly	Ala Val Gly Arg Ala	Ser
485		490	495
Trp Leu Tyr Lys	His Ile Phe Pro Phe	Ser Leu Ile Arg Tyr	Asp





<210> 104  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 104  
ggagaatgtg gccacaac 18

<210> 105  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 105  
gccctggcac agtgactcca tagacg 26

<210> 106  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 106  
atccacttca gcggacac 18

<210> 107  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 107  
ccagtgccag gatacctctc ttccccccag agcataacag acacg 45

<210> 108  
<211> 2579  
<212> DNA  
<213> Homo sapiens

<400> 108  
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acgcgcgcac acacactcgc tctcgcttgt ccatctccct cccgggggag 150  
ccggcgcgcg ctccacactt tgccgcacac tccggcgagc cgagcccgca 200

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Ser	Gln	Gln	Ser	Lys	Leu	Glu	Phe	Glu	Asn	Leu	Val	Glu	Glu	Thr	80	85	90
Ser	His	Phe	Val	Arg	Thr	Thr	Phe	Val	Ser	Arg	His	Lys	Lys	Phe	95	100	105
Asp	Glu	Phe	Phe	Arg	Glu	Leu	Leu	Glu	Asn	Ala	Glu	Lys	Ser	Leu	110	115	120
Asn	Asp	Met	Phe	Val	Arg	Thr	Tyr	Gly	Met	Leu	Tyr	Met	Gln	Asn	125	130	135
Ser	Glu	Val	Phe	Gln	Asp	Leu	Phe	Thr	Glu	Leu	Lys	Arg	Tyr	Tyr	140	145	150
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Ala	Arg	Leu	Leu	Glu	Arg	Met	Phe	Gln	Leu	Ile	Asn	Pro	Gln	Tyr	170	175	180
His	Phe	Ser	Glu	Asp	Tyr	Leu	Glu	Cys	Val	Ser	Lys	Tyr	Thr	Asp	185	190	195
Gln	Leu	Lys	Pro	Phe	Gly	Asp	Val	Pro	Arg	Lys	Leu	Lys	Ile	Gln	200	205	210
Val	Thr	Arg	Ala	Phe	Ile	Ala	Ala	Arg	Thr	Phe	Val	Gln	Gly	Leu	215	220	225
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Met	Gln	Val	Ser	Ala	Lys	Val	Phe	Gln	Gly	Cys	Gly	Gln	Pro	Lys	335	340	345
Pro	Ala	Pro	Ala	Leu	Arg	Ser	Ala	Arg	Ser	Ala	Pro	Glu	Asn	Phe	350	355	360
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 Trp Gly Gln Ala Leu Glu Glu Glu Glu Gly Ala Leu Leu Ala  
 50 55 60  
 Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser Gln  
 65 70 75  
 Pro His Leu Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp  
 80 85 90  
 Val Gly Tyr His Gly Ser Glu Ile Lys Thr Pro Thr Leu Asp Lys  
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Ile	His	Thr	Gly	Leu	Gln	His	Ser	Ile		Ile	Arg	Pro	Thr	Gln	Pro				
				140												150			
Asn	Cys	Leu	Pro	Leu	Asp	Asn	Ala	Thr		Leu	Pro	Gln	Lys	Leu	Lys				
				155												165			
Glu	Val	Gly	Tyr	Ser	Thr	His	Met	Val		Gly	Lys	Trp	His	Leu	Gly				
				170												180			
Phe	Asn	Arg	Lys	Glu	Cys	Met	Pro	Thr		Arg	Arg	Gly	Phe	Asp	Thr				
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Phe	Phe	Gly	Ser	Leu	Leu	Gly	Ser	Gly		Asp	Tyr	Tyr	Thr	His	Tyr				
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Lys	Cys	Asp	Ser	Pro	Gly	Met	Cys	Gly		Tyr	Asp	Leu	Tyr	Glu	Asn				
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Met	Tyr	Thr	Gln	Arg	Val	Gln	Gln	Ile		Leu	Ala	Ser	His	Asn	Pro				
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Thr	Lys	Pro	Ile	Phe	Leu	Tyr	Thr	Ala		Tyr	Gln	Ala	Val	His	Ser				
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Pro	Leu	Gln	Ala	Pro	Gly	Arg	Tyr	Phe		Glu	His	Tyr	Arg	Ser	Ile				
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Ile	Asn	Ile	Asn	Arg	Arg	Arg	Tyr	Ala		Ala	Met	Leu	Ser	Cys	Leu				
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Asp	Glu	Ala	Ile	Asn	Asn	Val	Thr	Leu		Ala	Leu	Lys	Thr	Tyr	Gly				
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Phe	Tyr	Asn	Asn	Ser	Ile	Ile	Ile	Tyr		Ser	Ser	Asp	Asn	Gly	Gly				
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Gln	Pro	Thr	Ala	Gly	Gly	Ser	Asn	Trp		Pro	Leu	Arg	Gly	Ser	Lys				
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Ser	Pro	Leu	Leu	Lys	Asn	Lys	Gly	Thr		Val	Cys	Lys	Glu	Leu	Val				
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His	Ile	Thr	Asp	Trp	Tyr	Pro	Thr	Leu		Ile	Ser	Leu	Ala	Glu	Gly				
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Gln	Ile	Asp	Glu	Asp	Ile	Gln	Leu	Asp		Gly	Tyr	Asp	Ile	Trp	Glu				
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Thr	Ile	Ser	Glu	Gly	Leu	Arg	Ser	Pro	Arg	Val	Asp	Ile	Leu	His
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Asn	Ile	Asp	Pro	Tyr	Thr	Pro	Arg	Gln	Lys	Met	Ala	Pro	Gly	Gln
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Gln	Ala	Met	Gly	Ser	Gly	Thr	Leu	Gln	Ser	Ser	Gln	Pro	Ser	Glu
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Cys	Ser	Thr	Gly	Asn	Cys	Leu	Gln	Glu	Ile	Leu	Ala	Thr	Ala	Thr
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Gly	Ser	Pro	Leu	Ser	Leu	Ser	Ala	Thr	Trp	Asp	Arg	Thr	Gly	Gly
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Ser	Thr	Ser	Gln	Pro	Thr	His	Met	Arg	Gly	Trp	Thr	Tyr	Leu	Thr
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Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	50	55	60
Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	65	70	75
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Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	95	100	105
Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	110	115	120
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Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	170	175	180
Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	185	190	195
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	200	205	210
Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	215	220	225
Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	230	235	240
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	245	250	255
Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	260	265	270
Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	275	280	285
His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	290	295	300
Pro	Glu	Pro	Thr	Arg	Thr	Pro	Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro			

	305		310		315
Phe Asn Tyr Glu	Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly				
	320		325		330
Gly Lys Lys Gly	Asn Glu Glu Lys				
	335				

<210> 120  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 120  
 cctcagtggc cacatgctca tg 22

<210> 121  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 121  
 ggctgcacgt atggctatcc atag 24

<210> 122  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 122  
 gataaactgt cagtacagct gtgaagacac agaagaagg ccacagtgcc 50

<210> 123  
 <211> 1199  
 <212> DNA  
 <213> Homo sapiens

<400> 123  
 gggagctgct gctgtggctg ctgggtgctgt gcgcgctgct cctgctcttg 50  
 gtgcagctgc tgcgcttcct gagggctgac ggcgacctga cgctactatg 100  
 ggccgagtgg cagggacgac gcccagaatg ggagctgact gatatggtgg 150  
 tgtgggtgac tggagcctcg agtgaattg gtgaggagct ggcttaccag 200  
 ttgtctaaac taggagtttc tcttgctgctg tcagccagaa gagtgcata 250  
 gctggaaagg gtgaaaagaa gatgcctaga gaatggcaat ttaaaagaaa 300

aagatatact tgttttgccc cttgacctga ccgacactgg ttcccatgaa 350  
gcggctacca aagctgttct ccaggagttt ggtagaatcg acattctggt 400  
caacaatggt ggaatgtccc agcgttctct gtgcatggat accagcttgg 450  
atgtctacag aaagctaata gagcttaact acttagggac ggtgtccttg 500  
acaaaatgtg ttctgcctca catgatogag aggaagcaag gaaagattgt 550  
tactgtgaat agcatcctgg gtatcatatc tgtacctctt tccattggat 600  
actgtgctag caagcatgct ctccgggggt tttttaatgg ccttcgaaca 650  
gaacttgcca catacccagg tataatagtt tctaacattt gcccaggacc 700  
tgtgcaatca aatattgtgg agaattccct agctggagaa gtcacaaaga 750  
ctataggcaa taatggagac cagtcccaca agatgacaac cagtcgttgt 800  
gtgcggctga tgttaatcag catggccaat gatttgaaag aagtttggat 850  
ctcagaacaa cctttcttgt tagtaacata tttgtggcaa tacatgcaa 900  
cctgggcctg gtggataacc aacaagatgg ggaagaaaag gattgagaac 950  
tttaagagtg gtgtggatgc agactcttct tattttaaaa tctttaagac 1000  
aaaacatgac tgaaaagagc acctgtactt ttcaagccac tggagggaga 1050  
aatggaaaac atgaaaacag caatcttctt atgcttctga ataatcaaag 1100  
actaatttgt gattttactt tttaatagat atgactttgc ttccaacatg 1150  
gaatgaaata aaaaataaat aataaaagat tgccatgaat cttgcaaaa 1199

<210> 124  
<211> 289  
<212> PRT  
<213> Homo sapiens

<400> 124  
Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu Glu  
1 5 10 15  
Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser  
20 25 30  
Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu  
35 40 45  
Glu Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu  
50 55 60  
Asp Leu Thr Asp Thr Gly Ser His Glu Ala Ala Thr Lys Ala Val  
65 70 75  
Leu Gln Glu Phe Gly Arg Ile Asp Ile Leu Val Asn Asn Gly Gly



	80		85		90
Met Ser Gln Arg	Ser Leu Cys Met Asp	Thr Ser Leu Asp Val Tyr			
	95	100			105
Arg Lys Leu Ile	Glu Leu Asn Tyr Leu	Gly Thr Val Ser Leu Thr			
	110	115			120
Lys Cys Val Leu	Pro His Met Ile Glu	Arg Lys Gln Gly Lys Ile			
	125	130			135
Val Thr Val Asn	Ser Ile Leu Gly Ile	Ile Ser Val Pro Leu Ser			
	140	145			150
Ile Gly Tyr Cys	Ala Ser Lys His Ala	Leu Arg Gly Phe Phe Asn			
	155	160			165
Gly Leu Arg Thr	Glu Leu Ala Thr Tyr	Pro Gly Ile Ile Val Ser			
	170	175			180
Asn Ile Cys Pro	Gly Pro Val Gln Ser	Asn Ile Val Glu Asn Ser			
	185	190			195
Leu Ala Gly Glu	Val Thr Lys Thr Ile	Gly Asn Asn Gly Asp Gln			
	200	205			210
Ser His Lys Met	Thr Thr Ser Arg Cys	Val Arg Leu Met Leu Ile			
	215	220			225
Ser Met Ala Asn	Asp Leu Lys Glu Val	Trp Ile Ser Glu Gln Pro			
	230	235			240
Phe Leu Leu Val	Thr Tyr Leu Trp Gln	Tyr Met Pro Thr Trp Ala			
	245	250			255
Trp Trp Ile Thr	Asn Lys Met Gly Lys	Lys Arg Ile Glu Asn Phe			
	260	265			270
Lys Ser Gly Val	Asp Ala Asp Ser Ser	Tyr Phe Lys Ile Phe Lys			
	275	280			285

Thr Lys His Asp

<210> 125  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 125  
 gcaatgaact gggagctgc 19

<210> 126  
 <211> 19  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

ctgtgaatag catcctggg 19

<210> 127

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 127

ctttcaagc cactggaggg 20

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 128

ctgtagacat ccaagctggt atcc 24

<210> 129

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 129

aagagtctgc atccacacca ctc 23

<210> 130

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 130

acctgacgct actatgggcc gagtggcagg gacgacgcc agaag 46

<210> 131

<211> 2365

<212> DNA

<213> Homo sapiens

<400> 131

ggcagctggg caccgccatc agctgttcgc gcgtcttctc ctccaggtgg 50  
 ggcaggggtt tcgggctggt ggagcatgtg ctgggacagg acagcatcct 100  
 caatcaatcc aacagcatat tcggttgcac cttctacaca ctacagctat 150  
 tgtaggttg cctgcggaca cgctgggcct ctgtcctgat gctgctgagc 200  
 tccctggtgt ctctcgtgg ttctgtctac ctggcctgga tcctgttctt 250  
 cgtgctctat gatttctgca ttgtttgtat caccacctat gctatcaacg 300  
 tgagcctgat gtggctcagt ttccggaagg tccaagaacc ccagggaag 350  
 gctaagaggc actgagccct caacccaagc caggctgacc tcctctgctt 400  
 tgctttggtc ttcaagccgc tcagcgtgcc tgtggacagc gtggccccgg 450  
 ccccccaag cctcaggagg gcaacacagt ccctggcgag tggccctggc 500  
 aggccagtgt gaggaggcaa ggagcccaca tctgcagcgg ctccctggtg 550  
 gcagacacct gggctctcac tgctgccac tgctttgaaa aggcagcagc 600  
 aacagaactg aattcctggt cagtggctct gggttctctg cagcgtgagg 650  
 gactcagccc tggggccgaa gaggtggggg tggctgccct gcagttgcc 700  
 agggcctata accactacag ccagggtca gacctggccc tgctgcagct 750  
 cgcccacccc acgaccaca caccctctg cctgcccag cccgccatc 800  
 gcttccctt tggagcctcc tgctgggcca ctggctggga tcaggacacc 850  
 agtgatgctc ctgggacct acgcaatctg cgctgcgtc tcctcagctg 900  
 cccacatgt aactgtatct acaaccagct gcaccagcga cacctgtcca 950  
 acccggcccg gcctgggatg ctatgtgggg gccccagcc tggggtgcag 1000  
 ggccctgtc agggagattc cgggggccct gtgtgtgcc tcgagcctga 1050  
 cggacactgg gttcaggctg gcacatcag ctttgcacat agctgtgcc 1100  
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 ctgcaggctc gagttcaggg ggcagcttct ctggcccaga gccagagac 1200  
 ccgggagatg agtgatgagg acagctgtgt agcctgtgga tccttgagga 1250  
 cagcaggtcc ccaggcagga gcaccctccc catggccctg ggaggccagg 1300  
 ctgatgcacc agggacagct ggcctgtggc ggagccctgg tgtcagagga 1350  
 ggcggtgcta actgtgccc actgcttcat tgggcgccag gccccagagg 1400  
 aatggagcgt agggctgggg accagaccgg aggagtgggg cctgaagcag 1450

ctcatcctgc atggagccta caccacacct gaggggggct acgacatggc 1500  
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tgaggtgagg ggcacatggt tcctggccgg gctgcacagc ttcggagatg 1850  
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ggacactccc acaccaact ctgctaccaa gcaggcgtct cagctttcct 2250  
cctcctttac tctttcagat acaatcacgc cagccacgtt gttttgaaa 2300  
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tgttacaaaa taaaa 2365

<210> 132  
<211> 571  
<212> PRT  
<213> Homo sapiens

<400> 132  
Met Leu Leu Ser Ser Leu Val Ser Leu Ala Gly Ser Val Tyr Leu  
1 5 10 15  
Ala Trp Ile Leu Phe Phe Val Leu Tyr Asp Phe Cys Ile Val Cys  
20 25 30  
Ile Thr Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe  
35 40 45  
Arg Lys Val Gln Glu Pro Gln Gly Lys Ala Lys Arg His Gly Asn  
50 55 60  
Thr Val Pro Gly Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln  
65 70 75

Gly Ala His Ile Cys Ser Gly Ser Leu Val Ala Asp Thr Trp Val  
 80 85 90  
 Leu Thr Ala Ala His Cys Phe Glu Lys Ala Ala Ala Thr Glu Leu  
 95 100 105  
 Asn Ser Trp Ser Val Val Leu Gly Ser Leu Gln Arg Glu Gly Leu  
 110 115 120  
 Ser Pro Gly Ala Glu Glu Val Gly Val Ala Ala Leu Gln Leu Pro  
 125 130 135  
 Arg Ala Tyr Asn His Tyr Ser Gln Gly Ser Asp Leu Ala Leu Leu  
 140 145 150  
 Gln Leu Ala His Pro Thr Thr His Thr Pro Leu Cys Leu Pro Gln  
 155 160 165  
 Pro Ala His Arg Phe Pro Phe Gly Ala Ser Cys Trp Ala Thr Gly  
 170 175 180  
 Trp Asp Gln Asp Thr Ser Asp Ala Pro Gly Thr Leu Arg Asn Leu  
 185 190 195  
 Arg Leu Arg Leu Ile Ser Arg Pro Thr Cys Asn Cys Ile Tyr Asn  
 200 205 210  
 Gln Leu His Gln Arg His Leu Ser Asn Pro Ala Arg Pro Gly Met  
 215 220 225  
 Leu Cys Gly Gly Pro Gln Pro Gly Val Gln Gly Pro Cys Gln Gly  
 230 235 240  
 Asp Ser Gly Gly Pro Val Leu Cys Leu Glu Pro Asp Gly His Trp  
 245 250 255  
 Val Gln Ala Gly Ile Ile Ser Phe Ala Ser Ser Cys Ala Gln Glu  
 260 265 270  
 Asp Ala Pro Val Leu Leu Thr Asn Thr Ala Ala His Ser Ser Trp  
 275 280 285  
 Leu Gln Ala Arg Val Gln Gly Ala Ala Phe Leu Ala Gln Ser Pro  
 290 295 300  
 Glu Thr Pro Glu Met Ser Asp Glu Asp Ser Cys Val Ala Cys Gly  
 305 310 315  
 Ser Leu Arg Thr Ala Gly Pro Gln Ala Gly Ala Pro Ser Pro Trp  
 320 325 330  
 Pro Trp Glu Ala Arg Leu Met His Gln Gly Gln Leu Ala Cys Gly  
 335 340 345  
 Gly Ala Leu Val Ser Glu Glu Ala Val Leu Thr Ala Ala His Cys  
 350 355 360  
 Phe Ile Gly Arg Gln Ala Pro Glu Glu Trp Ser Val Gly Leu Gly

	365		370		375
	Thr Arg Pro Glu	Glu Trp Gly Leu Lys	Gln Leu Ile Leu His	Gly	
	380		385		390
	Ala Tyr Thr His	Pro Glu Gly Gly Tyr	Asp Met Ala Leu Leu	Leu	
	395		400		405
	Leu Ala Gln Pro	Val Thr Leu Gly Ala	Ser Leu Arg Pro Leu	Cys	
	410		415		420
	Leu Pro Tyr Pro	Asp His His Leu Pro	Asp Gly Glu Arg Gly	Trp	
	425		430		435
	Val Leu Gly Arg	Ala Arg Pro Gly Ala	Gly Ile Ser Ser Leu	Gln	
	440		445		450
	Thr Val Pro Val	Thr Leu Leu Gly Pro	Arg Ala Cys Ser Arg	Leu	
	455		460		465
	His Ala Ala Pro	Gly Gly Asp Gly Ser	Pro Ile Leu Pro Gly	Met	
	470		475		480
	Val Cys Thr Ser	Ala Val Gly Glu Leu	Pro Ser Cys Glu Gly	Leu	
	485		490		495
	Ser Gly Ala Pro	Leu Val His Glu Val	Arg Gly Thr Trp Phe	Leu	
	500		505		510
	Ala Gly Leu His	Ser Phe Gly Asp Ala	Cys Gln Gly Pro Ala	Arg	
	515		520		525
	Pro Ala Val Phe	Thr Ala Leu Pro Ala	Tyr Glu Asp Trp Val	Ser	
	530		535		540
	Ser Leu Asp Trp	Gln Val Tyr Phe Ala	Glu Glu Pro Glu Pro	Glu	
	545		550		555
	Ala Glu Pro Gly	Ser Cys Leu Ala Asn	Ile Ser Gln Pro Thr	Ser	
	560		565		570

Cys

<210> 133  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 133  
 cctgtgctgt gcctcgagcc tgac 24

<210> 134  
 <211> 24  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gtgggcagca gttagcaccg cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 135

ggctggcatc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136

cgggccgccc ccggcccca ttcgggccgg gcctcgtgc ggcggcgact 50  
gagccaggct gggccgcgtc cctgagtccc agagtcggcg cggcgcggca 100  
ggggcagcct tccaccacgg ggagcccagc tgtcagccgc ctcacaggaa 150  
gatgctgcgt cggcggggca gccctggcat ggggtgcat gtgggtgcag 200  
ccctgggagc actgtggttc tgcctcacag gagccctgga ggtccaggtc 250  
cctgaagacc cagtgtggc actggtggc accgatgcca cctgtgctg 300  
ctccttctcc cctgagcctg gcttcagcct ggcacagctc aacctcatct 350  
ggcagctgac agatacaaaa cagctgtgac acagctttgc tgagggccag 400  
gaccaggga gcgcctatgc caaccgcacg gccctcttcc cggacctgct 450  
ggcacagggc aacgcattcc tgaggctgca gcgcgtgcgt gtggcggacg 500  
agggcagctt cacctgcttc gtgagcatcc gggatttcgg cagcgtgccc 550  
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tctgtcacca tcacagggca gcctatgaca ttccccccag aggccctgtg 900  
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gaccatgagg accagggagc tgctaccctt ccctacagct cctaccctct 1150  
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gcagccttat ttctccaatg gacatgattc ccaagtcata ctgctgcctt 1300  
ttttcttata gacacaatga acagaccacc cacaacctta gttctctaag 1350  
tcctcctgcc tgctgcctta ttccacagta catacatttc ttagggacac 1400  
agtacactga ccacatcacc accctcttct tccagtgtg cgtaggacat 1450  
ctggctgcct tttttctcca aaagatgcaa tattcagact gactgacccc 1500  
ctgccttatt tcaccaaaga cacgatgcat agtcaccccg gccttgtttc 1550  
tccaatggcc gtgatacact agtgatcatg ttcagccctg cttccacctg 1600  
catagaatct tttcttctca gacagggaca gtgcggcctc aacatctcct 1650  
ggagtctaga agctgtttcc tttcccttcc ttctcctctg ccccaagtga 1700  
agacagggca gggccaggaa tgctttgggg acaccgaggg gactgcccc 1750  
cacccccacc atggtgctat tctggggctg gggcagcttt ttctggctt 1800  
gcctctggcc agctcctggc ctctggtaga gtgagacttc agacgttctg 1850  
atgccttccg gatgtcatct ctccctgccc caggaatgga agatgtgagg 1900  
acttctaatt taaatgtggg actcggaggg attttgtaaa ctgggggtat 1950  
attttgggga aaataaatgt ctttgtaaaa aaaaaaaaaa aaaaaaaaaa 1998

<210> 137

<211> 316

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 233

<223> unknown amino acid

<400> 137

<400> 137  
Met Leu Arg Arg Arg Gly Ser Pro Gly Met Gly Val His Val Gly



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Ala Ala Leu Gly	Ala Leu Trp Phe Cys	Leu Thr Gly Ala Leu	Glu
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Val Gln Val Pro	Glu Asp Pro Val Val	Ala Leu Val Gly Thr	Asp
35		40	45
Ala Thr Leu Cys	Cys Ser Phe Ser Pro	Glu Pro Gly Phe Ser	Leu
50		55	60
Ala Gln Leu Asn	Leu Ile Trp Gln Leu	Thr Asp Thr Lys Gln	Leu
65		70	75
Val His Ser Phe	Ala Glu Gly Gln Asp	Gln Gly Ser Ala Tyr	Ala
80		85	90
Asn Arg Thr Ala	Leu Phe Pro Asp Leu	Leu Ala Gln Gly Asn	Ala
95		100	105
Ser Leu Arg Leu	Gln Arg Val Arg Val	Ala Asp Glu Gly Ser	Phe
110		115	120
Thr Cys Phe Val	Ser Ile Arg Asp Phe	Gly Ser Ala Ala Val	Ser
125		130	135
Leu Gln Val Ala	Ala Pro Tyr Ser Lys	Pro Ser Met Thr Leu	Glu
140		145	150
Pro Asn Lys Asp	Leu Arg Pro Gly Asp	Thr Val Thr Ile Thr	Cys
155		160	165
Ser Ser Tyr Gln	Gly Tyr Pro Glu Ala	Glu Val Phe Trp Gln	Asp
170		175	180
Gly Gln Gly Val	Pro Leu Thr Gly Asn	Val Thr Thr Ser Gln	Met
185		190	195
Ala Asn Glu Gln	Gly Leu Phe Asp Val	His Ser Val Leu Arg	Val
200		205	210
Val Leu Gly Ala	Asn Gly Thr Tyr Ser	Cys Leu Val Arg Asn	Pro
215		220	225
Val Leu Gln Gln	Asp Ala His Xaa Ser	Val Thr Ile Thr Gly	Gln
230		235	240
Pro Met Thr Phe	Pro Pro Glu Ala Leu	Trp Val Thr Val Gly	Leu
245		250	255
Ser Val Cys Leu	Ile Ala Leu Leu Val	Ala Leu Ala Phe Val	Cys
260		265	270
Trp Arg Lys Ile	Lys Gln Ser Cys Glu	Glu Glu Asn Ala Gly	Ala
275		280	285
Glu Asp Gln Asp	Gly Glu Gly Glu Gly	Ser Lys Thr Ala Leu	Gln
290		295	300

Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile  
 305 310 315

Ala

<210> 138  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 138  
 ctggcacagc tcaacctcat ctgg 24

<210> 139  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 139  
 gctgtctgtc tgtctcattg 20

<210> 140  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 140  
 ggacacagta tactgaccac 20

<210> 141  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 141  
 tgcgaaccag gcagctgtaa gtgc 24

<210> 142  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 142  
tggaagaaga ggggtggtgat gtgg 24

<210> 143  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 143  
cagctgacag acaccaaaca gctggtgcac agtttcaccg aaggc 45

<210> 144  
<211> 2336  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1620, 1673  
<223> unknown base

<400> 144  
ttcgtgaccc ttgagaaaag agttggtggt aaatgtgcc cgtcttctaa 50  
gaagggggag tcttgaactt gtctgaagcc cttgtccgta agccttgaac 100  
tacgtttctta aatctatgaa gtcgaggac ctttcgctgc tttttaggg 150  
acttctttcc ttgcttcagc aacatgaggc ttttcttggtg gaacgcggtc 200  
ttgactctgt tcgtcacttc tttgattggg gctttgatcc ctgaaccaga 250  
agtgaataatt gaagttctcc agaagccatt catctgccat cgcaagacca 300  
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gtttaccctg ggcctcctgg aggctctcaa aggttgggac cagggttgga 450  
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gttaaagcat atttaaagaa ggagtttgaa aaacatggtg cgggtggtgaa 700  
tgaaagtcac catgatgctt tgggtggagga tatttttgat aaagaagatg 750  
aagacaaaga tgggtttata tctgccagag aatttacata taaacacgat 800  
gagttataga gatacatcta cccttttaaat atagcactca tctttcaaga 850

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tgctttgttt tttattttta tatatttttt ctgactocta tttaaagaac 950  
cccttaggtt tctaagtacc catttctttc tgataagtta ttgggaagaa 1000  
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caactgggaa tataccacga catgagacca gggtatagca caaattagca 1150  
ccctatattt ctgcttcctt ctattttctc caagttagag gtcaacattt 1200  
gaaaagcctt ttgcaatagc ccaaggcttg ctattttcat gttataatga 1250  
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tcacttgaga tcaggagttc aagaccagcc tggccaacat ggtgaaacct 2100  
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aggcggaggt tgcagtgagc caagattgtg ccaactgcact ccagcctggg 2250  
tgacagagca agactccatc tcaaaaaaaa aaaaaagaag cagacctaca 2300

gcagctacta ttgaataaat acctatcctg gatttt 2336

<210> 145

<211> 211

<212> PRT

<213> Homo sapiens

<400> 145

Met Arg Leu Phe Leu Trp Asn Ala Val Leu Thr Leu Phe Val Thr  
1 5 10 15

Ser Leu Ile Gly Ala Leu Ile Pro Glu Pro Glu Val Lys Ile Glu  
20 25 30

Val Leu Gln Lys Pro Phe Ile Cys His Arg Lys Thr Lys Gly Gly  
35 40 45

Asp Leu Met Leu Val His Tyr Glu Gly Tyr Leu Glu Lys Asp Gly  
50 55 60

Ser Leu Phe His Ser Thr His Lys His Asn Asn Gly Gln Pro Ile  
65 70 75

Trp Phe Thr Leu Gly Ile Leu Glu Ala Leu Lys Gly Trp Asp Gln  
80 85 90

Gly Leu Lys Gly Met Cys Val Gly Glu Lys Arg Lys Leu Ile Ile  
95 100 105

Pro Pro Ala Leu Gly Tyr Gly Lys Glu Gly Lys Gly Lys Ile Pro  
110 115 120

Pro Glu Ser Thr Leu Ile Phe Asn Ile Asp Leu Leu Glu Ile Arg  
125 130 135

Asn Gly Pro Arg Ser His Glu Ser Phe Gln Glu Met Asp Leu Asn  
140 145 150

Asp Asp Trp Lys Leu Ser Lys Asp Glu Val Lys Ala Tyr Leu Lys  
155 160 165

Lys Glu Phe Glu Lys His Gly Ala Val Val Asn Glu Ser His His  
170 175 180

Asp Ala Leu Val Glu Asp Ile Phe Asp Lys Glu Asp Glu Asp Lys  
185 190 195

Asp Gly Phe Ile Ser Ala Arg Glu Phe Thr Tyr Lys His Asp Glu  
200 205 210

Leu

<210> 146

<211> 26

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 146  
ctttccttgc ttcagcaaca tgaggc 26

<210> 147  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 147  
gcccagagca ggaggaatga tgagc 25

<210> 148  
<211> 49  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 148  
gtggaacgcg gtcttgactc tgttcgtcac ttctttgatt ggggctttg 49

<210> 149  
<211> 2196  
<212> DNA  
<213> Homo sapiens

<400> 149  
aataaagctt ccttaatggt gtatatgtct ttgaagtaca tccgtgcatt 50  
tttttttagc atccaaccat tctcccttg tagttctcgc cccctcaaatt 100  
caccctctcc cgtagccac ccgactaaca tctcagtcgc tgaaaatgca 150  
cagagatgcc tggtacctc gccctgcctt cagcctcacg gggctcagtc 200  
tctttttctc ttgggtgccca ccaggacgga gcatggaggt cacagtacct 250  
gccaccctca acgtctcaa tggctctgac gcccgctgc cctgcacctt 300  
caactcctgc tacacagtga accacaaaca gttctccctg aactggactt 350  
accaggagtg caacaactgc tctgaggaga tgttcctcca gttccgcatg 400  
aagatcatta acctgaagct ggagcggttt caagaccgcg tggagttctc 450  
aggggaacccc agcaagtacg atgtgtcggg gatgctgaga aacgtgcagc 500  
cggaggatga ggggatttac aactgctaca tcatgaaccc ccctgaccgc 550  
caccgtggcc atggcaagat ccatctgcag gtcctcatgg aagagcccc 600



cgtgtgcctg taatcccagc tatttgggag gctgaggcag gagaatcgct 2100  
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 tgcaattcag cctgggtgac atagagagac tccatctcaa aaaaaa 2196

<210> 150  
 <211> 215  
 <212> PRT  
 <213> Homo sapiens

<400> 150  
 Met His Arg Asp Ala Trp Leu Pro Arg Pro Ala Phe Ser Leu Thr  
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 Gly Leu Ser Leu Phe Phe Ser Leu Val Pro Pro Gly Arg Ser Met  
 20 25 30  
 Glu Val Thr Val Pro Ala Thr Leu Asn Val Leu Asn Gly Ser Asp  
 35 40 45  
 Ala Arg Leu Pro Cys Thr Phe Asn Ser Cys Tyr Thr Val Asn His  
 50 55 60  
 Lys Gln Phe Ser Leu Asn Trp Thr Tyr Gln Glu Cys Asn Asn Cys  
 65 70 75  
 Ser Glu Glu Met Phe Leu Gln Phe Arg Met Lys Ile Ile Asn Leu  
 80 85 90  
 Lys Leu Glu Arg Phe Gln Asp Arg Val Glu Phe Ser Gly Asn Pro  
 95 100 105  
 Ser Lys Tyr Asp Val Ser Val Met Leu Arg Asn Val Gln Pro Glu  
 110 115 120  
 Asp Glu Gly Ile Tyr Asn Cys Tyr Ile Met Asn Pro Pro Asp Arg  
 125 130 135  
 His Arg Gly His Gly Lys Ile His Leu Gln Val Leu Met Glu Glu  
 140 145 150  
 Pro Pro Glu Arg Asp Ser Thr Val Ala Val Ile Val Gly Ala Ser  
 155 160 165  
 Val Gly Gly Phe Leu Ala Val Val Ile Leu Val Leu Met Val Val  
 170 175 180  
 Lys Cys Val Arg Arg Lys Lys Glu Gln Lys Leu Ser Thr Asp Asp  
 185 190 195  
 Leu Lys Thr Glu Glu Glu Gly Lys Thr Asp Gly Glu Gly Asn Pro  
 200 205 210  
 Asp Asp Gly Ala Lys  
 215

<210> 151



<211> 524  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 103, 233  
<223> unknown base

<400> 151  
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ccnactaaca tctcagtctc tgaaaatgca cagagatgcc tggctacctc 150  
gccctgcctt cagcctcagc gggctcagtc tctttttctc tttggtgcc 200  
ccaggacgga gcatggaggt ccacagtacc tgnccaccct caacgtctc 250  
aatggctctg acgcccgcct gccctgcct tcaactcctg ctacacagtg 300  
aaccacaaac agttctccct gaactggact taccaggagt gcaacaactg 350  
ctctgaggag atgttctcc agttccgcat gaagatcatt aacctgaagc 400  
tgagcggtt tcaagaccgc gtggagttct cagggaaccc cagcaagtac 450  
gatgtgtcgg tgatgctgag aaacgtgcag ccggaggatg aggggattta 500  
caactgctac atcatgaacc cccc 524

<210> 152  
<211> 368  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 56, 123  
<223> unknown base

<400> 152  
tcacggggct catctctttt tctctttggt gccaccagg acggagcatg 50  
gaggtncaca tacctgccac cctcaacgtc ctcaatggct ttgacgccg 100  
cctgccctgc accttcaact cngctacac agtgaaccac aaacagttct 150  
ccctgaactg gatttaccag gagtgaaca actggctctg aggagatgtt 200  
cctccagttc ccgcatggaa gatcatttaa cctgaaagct ggaagcggtt 250  
ttcaagaacc gcgtggaagt ttctcagga accccagcaa gtacgatgtg 300  
tcggtgatgc tgagaaacgt gcagccggag gatgagggga ttacaactg 350  
ctacatcatg aaccccc 368

<210> 153  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 153  
 acggagcatg gaggtccaca gtac 24

<210> 154  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 154  
 gcacgtttct cagcatcacc gac 23

TOPCAT = TBOC

<210> 155  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 155  
 cgctgcccct gcaccttcaa ctctgctac acagtgaacc acaaacagtt 50

<210> 156  
 <211> 2680  
 <212> DNA  
 <213> Homo sapiens

<400> 156  
 tggggcgacc gtcgtacacc atgggacctc acctccgccc ctaccgtgtg 50  
 gggctgctcc cggatggcct cctgttcctc ttgctgctgc taatgctgct 100  
 cgcggaccca gcgctcccg cgggacgtca cccccagtg gtgctggtcc 150  
 ctggtgattt gggtaaccaa ctggaagcca agctggacaa gccgacagtg 200  
 gtgcactacc tctgctocaa gaagaccgaa agctacttca caatctggct 250  
 gaacctggaa ctgctgctgc ctgtcatcat tgactgctgg attgacaata 300  
 tcaggctggg ttacaacaaa acatccaggg ccaccagtt tctgatggg 350  
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 ggacccagc aaaagcagcg tgggttcta tttccacacc atggtggaga 450  
 gccttgtggg ctgggggtac acacggggtg aggatgtccg aggggctccc 500

tatgactggc gccgagcccc aatgaaaac gggccctact tcctggccct 550  
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 cagccgcagg cctggaagga caagtatatc cgggccttcg tgtcactggg 700  
 tgcgccctgg gggggcgtgg ccaagaccct gcgcgtcctg gcttcaggag 750  
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 actaccgcaa gttcttcag gacatcggt ttgaagatgg ctggctcatg 950  
 cggcaggaca cagaagggt ggtggaagcc acgatgccac ctggcgtgca 1000  
 gctgcactgc ctctatgta ctggcgtccc cacaccagac tccttctact 1050  
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 ggtactgtga acttgaagag tgccctgcag tgccaggcct ggcagagccg 1150  
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 aagtgtgtt tggtatcctt tctctgtggc agtgaagaag gaagaaatga 1450  
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cccccagtcc cgcaggtgt gttccaggg ccctgatttc ctggatgtg 2000  
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 atgctgtaaa aaaaaaaaaa aaaaaaaaaa 2680

<210> 157  
 <211> 412  
 <212> PRT  
 <213> Artificial

<400> 157  
 Met Gly Leu His Leu Arg Pro Tyr Arg Val Gly Leu Leu Pro Asp  
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 Gly Leu Leu Phe Leu Leu Leu Leu Met Leu Leu Ala Asp Pro  
 20 25 30  
 Ala Leu Pro Ala Gly Arg His Pro Pro Val Val Leu Val Pro Gly  
 35 40 45  
 Asp Leu Gly Asn Gln Leu Glu Ala Lys Leu Asp Lys Pro Thr Val  
 50 55 60  
 Val His Tyr Leu Cys Ser Lys Lys Thr Glu Ser Tyr Phe Thr Ile  
 65 70 75  
 Trp Leu Asn Leu Glu Leu Leu Leu Pro Val Ile Ile Asp Cys Trp  
 80 85 90  
 Ile Asp Asn Ile Arg Leu Val Tyr Asn Lys Thr Ser Arg Ala Thr  
 95 100 105  
 Gln Phe Pro Asp Gly Val Asp Val Arg Val Pro Gly Phe Gly Lys

	110	115	120
Thr Phe Ser Leu	Glu Phe Leu Asp Pro	Ser Lys Ser Ser Val Gly	135
	125	130	
Ser Tyr Phe His	Thr Met Val Glu Ser Leu Val Gly Trp Gly Tyr		150
	140	145	
Thr Arg Gly Glu Asp Val Arg Gly Ala Pro Tyr Asp Trp Arg Arg			165
	155	160	
Ala Pro Asn Glu Asn Gly Pro Tyr Phe Leu Ala Leu Arg Glu Met			180
	170	175	
Ile Glu Glu Met Tyr Gln Leu Tyr Gly Gly Pro Val Val Leu Val			195
	185	190	
Ala His Ser Met Gly Asn Met Tyr Thr Leu Tyr Phe Leu Gln Arg			210
	200	205	
Gln Pro Gln Ala Trp Lys Asp Lys Tyr Ile Arg Ala Phe Val Ser			225
	215	220	
Leu Gly Ala Pro Trp Gly Gly Val Ala Lys Thr Leu Arg Val Leu			240
	230	235	
Ala Ser Gly Asp Asn Asn Arg Ile Pro Val Ile Gly Pro Leu Lys			255
	245	250	
Ile Arg Glu Gln Gln Arg Ser Ala Val Ser Thr Ser Trp Leu Leu			270
	260	265	
Pro Tyr Asn Tyr Thr Trp Ser Pro Glu Lys Val Phe Val Gln Thr			285
	275	280	
Pro Thr Ile Asn Tyr Thr Leu Arg Asp Tyr Arg Lys Phe Phe Gln			300
	290	295	
Asp Ile Gly Phe Glu Asp Gly Trp Leu Met Arg Gln Asp Thr Glu			315
	305	310	
Gly Leu Val Glu Ala Thr Met Pro Pro Gly Val Gln Leu His Cys			330
	320	325	
Leu Tyr Gly Thr Gly Val Pro Thr Pro Asp Ser Phe Tyr Tyr Glu			345
	335	340	
Ser Phe Pro Asp Arg Asp Pro Lys Ile Cys Phe Gly Asp Gly Asp			360
	350	355	
Gly Thr Val Asn Leu Lys Ser Ala Leu Gln Cys Gln Ala Trp Gln			375
	365	370	
Ser Arg Gln Glu His Gln Val Leu Leu Gln Glu Leu Pro Gly Ser			390
	380	385	
Glu His Ile Glu Met Leu Ala Asn Ala Thr Thr Leu Ala Tyr Leu			405
	395	400	

Lys Arg Val Leu Leu Gly Pro  
410

<210> 158  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 158  
ctggggctac acacggggtg agg 23

<210> 159  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 159  
ggtgccgctg cagaaagtag agcg 24

<210> 160  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 160  
gccccaaatg aaaacgggcc ctacttcctg gccctccgcg agatg 45

<210> 161  
<211> 1512  
<212> DNA  
<213> Homo sapiens

<400> 161  
cgacgcgctg ggcggacgcg tggggcggcg gcagcggcgg cgacggcgac 50  
atggagagcg gggcctacgg cgcgccaag gcgggaggct ccttcgacct 100  
gcggcgcttc ctgacgcagc cgcaggtggt ggcgcgcgcc gtgtgcttgg 150  
tcttcgcctt gatcgtgttc tcttgcattc atggtgaggg ctacagcaat 200  
gcccacgagt ctaagcagat gtactgcgtg ttcaaccgca acgaggatgc 250  
ctgccgctat ggcagtgcca tcgggggtgct ggccttcctg gcctcggcct 300  
tcttcttggt ggtcgacgcg tatttcccc agatcagcaa cgccactgac 350  
cgcaagtacc tggtcattgg tgacctgctc ttctcagctc tctggacctt 400

cctgtggttt gttggtttct gcttcctcac caaccagtgg gcagtcacca 450  
 acccgaagga cgtgctggtg ggggccgact ctgtgagggc agccatcacc 500  
 ttcagcttct tttccatctt ctctggggt gtgctggcct ccctggccta 550  
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 ccaactccga cccaacact gcctacgcct cctaccagg tgcatctgtg 650  
 gacaactacc aacagccacc cttcaccag aacgcggaga ccaccgagg 700  
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 ctgccagccc ctctctttca cctgttccat cctgtgcagc tgacacacag 850  
 ctaaggagcc tcatagcctg gcgggggctg gcagagccac accccaagt 900  
 cctgtgcca gagggcttca gtcagccgt cactcctca gggcactttt 950  
 aggaaaggg ttttagctag tgtttttct cgcttttaac gacctcagcc 1000  
 ccgcctgcag tggctagaag ccagcaggtg cccatgtgct actgacaagt 1050  
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 gcgttctctg ccaaagactc gtgggggcca tcacacctgc cctgtgcagc 1150  
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 ccaactgctg atgatctggg ggccaccacc ctgtgccgtt ggctctggg 1250  
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 ttatgtaa atctctgagt tgttacttag gaagcctggg gagggcagg 1400  
 gtgccccatg gctcccagac totgtctgtg ccgagtgtat tataaatcg 1450  
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 tctcattcaa ag 1512

<210> 162  
 <211> 224  
 <212> PRT  
 <213> Homo sapiens

<400> 162  
 Met Glu Ser Gly Ala Tyr Gly Ala Ala Lys Ala Gly Gly Ser Phe  
 1 5 10 15  
 Asp Leu Arg Arg Phe Leu Thr Gln Pro Gln Val Val Ala Arg Ala  
 20 25 30

Val Cys Leu Val Phe Ala Leu Ile Val Phe Ser Cys Ile Tyr Gly  
                   35                  40                  45  
 Glu Gly Tyr Ser Asn Ala His Glu Ser Lys Gln Met Tyr Cys Val  
                   50                  55                  60  
 Phe Asn Arg Asn Glu Asp Ala Cys Arg Tyr Gly Ser Ala Ile Gly  
                   65                  70                  75  
 Val Leu Ala Phe Leu Ala Ser Ala Phe Phe Leu Val Val Asp Ala  
                   80                  85                  90  
 Tyr Phe Pro Gln Ile Ser Asn Ala Thr Asp Arg Lys Tyr Leu Val  
                   95                  100                 105  
 Ile Gly Asp Leu Leu Phe Ser Ala Leu Trp Thr Phe Leu Trp Phe  
                  110                 115                 120  
 Val Gly Phe Cys Phe Leu Thr Asn Gln Trp Ala Val Thr Asn Pro  
                  125                 130                 135  
 Lys Asp Val Leu Val Gly Ala Asp Ser Val Arg Ala Ala Ile Thr  
                  140                 145                 150  
 Phe Ser Phe Phe Ser Ile Phe Ser Trp Gly Val Leu Ala Ser Leu  
                  155                 160                 165  
 Ala Tyr Gln Arg Tyr Lys Ala Gly Val Asp Asp Phe Ile Gln Asn  
                  170                 175                 180  
 Tyr Val Asp Pro Thr Pro Asp Pro Asn Thr Ala Tyr Ala Ser Tyr  
                  185                 190                 195  
 Pro Gly Ala Ser Val Asp Asn Tyr Gln Gln Pro Pro Phe Thr Gln  
                  200                 205                 210  
 Asn Ala Glu Thr Thr Glu Gly Tyr Gln Pro Pro Pro Val Tyr  
                  215                 220

<210> 163  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 163  
 tggctcttcgc cttgatcgtg ttct 24

<210> 164  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe



<400> 164  
gtgtactgag cggcggtag 20

<210> 165  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 165  
ctgaaggtag tggctgccct cac 23

<210> 166  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 166  
ccaggaggct catgggaaag tcc 23

<210> 167  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 167  
ccacgagtct aagcagatgt actgctgtgt caaccgcaac gaggatgcct 50

<210> 168  
<211> 3143  
<212> DNA  
<213> Homo sapiens

<400> 168  
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ctggcgggca gggggacgga ggtgatggcg aggaagcgga gccagagggg 150  
atgttcaagg cctgtgagga ctccaagaga aaagcccggg gctacctccg 200  
cctggtgccc ctgtttgtgc tgctggccct gctcgtgctg gcttcggcgg 250  
gggtgtact ctggtatttc ctagggtaca aggcggaggt gatggtcagc 300  
caggtgtact caggcagtct gcgtgtactc aatgccact tctcccagga 350  
tcttaccgcg cggaatcta gtgccttccg cagtgaacc gccaaagccc 400

agaagatgct caaggagctc atcaccagca cccgcctggg aacttactac 450  
 aactccagct ccgtctattc ctttggggag ggacccctca cctgcttctt 500  
 ctgggttcatt ctccaaatcc ccgagcaccg ccggctgatg ctgagccccg 550  
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 gcagcgatga agagcagtgc caggaagggg tgccatgtgg gacattcacc 1650  
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 tgggcggccc gactgcaggg acggctcgga tgaggagcac tgtgactgtg 1750  
 gcctccaggg cccctccagc cgcattgttg gtggagctgt gtcctccag 1800  
 ggtgagtggc catggcaggc cagcctccag gttcggggtc gacacatctg 1850

total: 4302 bp

tgggggggcc ctcatcgctg accgctgggt gataacagct gccactgct 1900  
tccaggagga cagcatggcc tccacggggtg tgtggaccgt gttcctgggc 1950  
aaggtgtggc agaactcgcg ctggcctgga gaggtgtcct tcaaggtgag 2000  
ccgcctgctc ctgcacccgt accacgaaga ggacagccat gactacgacg 2050  
tggcgctgct gcagctcgac caccgggtgg tgcgctcggc cgccgtgcgc 2100  
cccgtctgcc tgcccgcgcg ctcccacttc ttcgagccg gcctgcactg 2150  
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tttgaataa agctgcctga tcaaaaaaaaa aaaaaaaaaa aaa 3143

<210> 169  
<211> 802  
<212> PRT  
<213> Homo sapiens  
  
<400> 169

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Cys	Glu	Asp	Ser	Lys	Arg	Lys	Ala	Arg	Gly	Tyr	Leu	Arg	Leu	Val	35	40	45	
Pro	Leu	Phe	Val	Leu	Leu	Ala	Leu	Leu	Val	Leu	Ala	Ser	Ala	Gly	50	55	60	
Val	Leu	Leu	Trp	Tyr	Phe	Leu	Gly	Tyr	Lys	Ala	Glu	Val	Met	Val	65	70	75	
Ser	Gln	Val	Tyr	Ser	Gly	Ser	Leu	Arg	Val	Leu	Asn	Arg	His	Phe	80	85	90	
Ser	Gln	Asp	Leu	Thr	Arg	Arg	Glu	Ser	Ser	Ala	Phe	Arg	Ser	Glu	95	100	105	
Thr	Ala	Lys	Ala	Gln	Lys	Met	Leu	Lys	Glu	Leu	Ile	Thr	Ser	Thr	110	115	120	
Arg	Leu	Gly	Thr	Tyr	Tyr	Asn	Ser	Ser	Ser	Val	Tyr	Ser	Phe	Gly	125	130	135	
Glu	Gly	Pro	Leu	Thr	Cys	Phe	Phe	Trp	Phe	Ile	Leu	Gln	Ile	Pro	140	145	150	
Glu	His	Arg	Arg	Leu	Met	Leu	Ser	Pro	Glu	Val	Val	Gln	Ala	Leu	155	160	165	
Leu	Val	Glu	Glu	Leu	Leu	Ser	Thr	Val	Asn	Ser	Ser	Ala	Ala	Val	170	175	180	
Pro	Tyr	Arg	Ala	Glu	Tyr	Glu	Val	Asp	Pro	Glu	Gly	Leu	Val	Ile	185	190	195	
Leu	Glu	Ala	Ser	Val	Lys	Asp	Ile	Ala	Ala	Leu	Asn	Ser	Thr	Leu	200	205	210	
Gly	Cys	Tyr	Arg	Tyr	Ser	Tyr	Val	Gly	Gln	Gly	Gln	Val	Leu	Arg	215	220	225	
Leu	Lys	Gly	Pro	Asp	His	Leu	Ala	Ser	Ser	Cys	Leu	Trp	His	Leu	230	235	240	
Gln	Gly	Pro	Lys	Asp	Leu	Met	Leu	Lys	Leu	Arg	Leu	Glu	Trp	Thr	245	250	255	
Leu	Ala	Glu	Cys	Arg	Asp	Arg	Leu	Ala	Met	Tyr	Asp	Val	Ala	Gly	260	265	270	
Pro	Leu	Glu	Lys	Arg	Leu	Ile	Thr	Ser	Val	Tyr	Gly	Cys	Ser	Arg	275	280	285	
Gln	Glu	Pro	Val	Val	Glu	Val	Leu	Ala	Ser	Gly	Ala	Ile	Met	Ala				

290										295					300				
Val	Val	Trp	Lys	Lys	Gly	Leu	His	Ser	Tyr	Tyr	Asp	Pro	Phe	Val					
				305					310					315					
Leu	Ser	Val	Gln	Pro	Val	Val	Phe	Gln	Ala	Cys	Glu	Val	Asn	Leu					
				320					325					330					
Thr	Leu	Asp	Asn	Arg	Leu	Asp	Ser	Gln	Gly	Val	Leu	Ser	Thr	Pro					
				335					340					345					
Tyr	Phe	Pro	Ser	Tyr	Tyr	Ser	Pro	Gln	Thr	His	Cys	Ser	Trp	His					
				350					355					360					
Leu	Thr	Val	Pro	Ser	Leu	Asp	Tyr	Gly	Leu	Ala	Leu	Trp	Phe	Asp					
				365					370					375					
Ala	Tyr	Ala	Leu	Arg	Arg	Gln	Lys	Tyr	Asp	Leu	Pro	Cys	Thr	Gln					
				380					385					390					
Gly	Gln	Trp	Thr	Ile	Gln	Asn	Arg	Arg	Leu	Cys	Gly	Leu	Arg	Ile					
				395					400					405					
Leu	Gln	Pro	Tyr	Ala	Glu	Arg	Ile	Pro	Val	Val	Ala	Thr	Ala	Gly					
				410					415					420					
Ile	Thr	Ile	Asn	Phe	Thr	Ser	Gln	Ile	Ser	Leu	Thr	Gly	Pro	Gly					
				425					430					435					
Val	Arg	Val	His	Tyr	Gly	Leu	Tyr	Asn	Gln	Ser	Asp	Pro	Cys	Pro					
				440					445					450					
Gly	Glu	Phe	Leu	Cys	Ser	Val	Asn	Gly	Leu	Cys	Val	Pro	Ala	Cys					
				455					460					465					
Asp	Gly	Val	Lys	Asp	Cys	Pro	Asn	Gly	Leu	Asp	Glu	Arg	Asn	Cys					
				470					475					480					
Val	Cys	Arg	Ala	Thr	Phe	Gln	Cys	Lys	Glu	Asp	Ser	Thr	Cys	Ile					
				485					490					495					
Ser	Leu	Pro	Lys	Val	Cys	Asp	Gly	Gln	Pro	Asp	Cys	Leu	Asn	Gly					
				500					505					510					
Ser	Asp	Glu	Glu	Gln	Cys	Gln	Glu	Gly	Val	Pro	Cys	Gly	Thr	Phe					
				515					520					525					
Thr	Phe	Gln	Cys	Glu	Asp	Arg	Ser	Cys	Val	Lys	Lys	Pro	Asn	Pro					
				530					535					540					
Gln	Cys	Asp	Gly	Arg	Pro	Asp	Cys	Arg	Asp	Gly	Ser	Asp	Glu	Glu					
				545					550					555					
His	Cys	Asp	Cys	Gly	Leu	Gln	Gly	Pro	Ser	Ser	Arg	Ile	Val	Gly					
				560					565					570					
Gly	Ala	Val	Ser	Ser	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu					
				575					580					585					

Gln Val Arg Gly Arg His Ile Cys Gly Gly Ala Leu Ile Ala Asp  
590 595 600

Arg Trp Val Ile Thr Ala Ala His Cys Phe Gln Glu Asp Ser Met  
605 610 615

Ala Ser Thr Val Leu Trp Thr Val Phe Leu Gly Lys Val Trp Gln  
620 625 630

Asn Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser Arg Leu  
635 640 645

Leu Leu His Pro Tyr His Glu Glu Asp Ser His Asp Tyr Asp Val  
650 655 660

Ala Leu Leu Gln Leu Asp His Pro Val Val Arg Ser Ala Ala Val  
665 670 675

Arg Pro Val Cys Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly  
680 685 690

Leu His Cys Trp Ile Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly  
695 700 705

Pro Ile Ser Asn Ala Leu Gln Lys Val Asp Val Gln Leu Ile Pro  
710 715 720

Gln Asp Leu Cys Ser Glu Ala Tyr Arg Tyr Gln Val Thr Pro Arg  
725 730 735

Met Leu Cys Ala Gly Tyr Arg Lys Gly Lys Lys Asp Ala Cys Gln  
740 745 750

Gly Asp Ser Gly Gly Pro Leu Val Cys Lys Ala Leu Ser Gly Arg  
755 760 765

Trp Phe Leu Ala Gly Leu Val Ser Trp Gly Leu Gly Cys Gly Arg  
770 775 780

Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr Gly Val Ile Ser  
785 790 795

Trp Ile Gln Gln Val Val Thr  
800

<210> 170  
<211> 1327  
<212> DNA  
<213> Homo sapiens

<400> 170  
gcacccaggg ccagtggacg atccagaaca ggaggctgtg tggttgccg 50  
atcctgcagc cctacgccga gaggatcccc gtggtggcca cggccgggat 100  
caccatcaac ttcacctccc agatctccct caccgggccc ggtgtgcggg 150  
tgcaactatgg cttgtacaac cagtgcggacc cctgccctgg agagttcctc 200

tgttctgtga atggactctg tgtccctgcc tgtgatggg tcaaggactg 250  
 ccccaacggc ctggatgaga gaaactgctg ttgcagagcc acattccagt 300  
 gcaaagagga cagcacatgc atctcactgc ccaaggtctg tgatgggcag 350  
 cctgattgtc tcaacggcag cgatgaagag cagtgccagg aaggggtgcc 400  
 atgtgggaca ttacacttcc agtgtgagga ccggagctgc gtgaagaagc 450  
 ccaacccgca gtgtgatggg cggcccgcact gcagggacgg ctccgatgag 500  
 gagcactgtg actgtggcct ccagggcccc tccagccgca ttgttggtgg 550  
 agctgtgtcc tccgaggggt agtgccatg gcaggccagc ctccaggttc 600  
 ggggtcgaca catctgtggg gggggccctca tcgctgaccg ctgggtgata 650  
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 gaccgtgttc ctgggcaagg tgtggcagaa ctgcgcgtgg cctggagagg 750  
 tgtccttcaa ggtgagccgc ctgctcctgc acccgtagca cgaagaggac 800  
 agccatgact acgacgtggc gctgctgcag ctgcaccacc cgggtggtgcg 850  
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 gtgccggcta ccgcaagggc aagaaggatg cctgtcaggg tgactcaggt 1100  
 ggtccgctgg tgtgcaaggc actcagtggc cgctgggttc tggcggggct 1150  
 ggtcagctgg ggcctgggct gtggccggcc taactacttc ggcgtctaca 1200  
 cccgcattac aggtgtgatc agctggatcc agcaagtggg gacctgagga 1250  
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 gcaactgcca agcaggggga caagtat 1327

<210> 171

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

taacagctgc ccaactgcttc cagg 24

<210> 172

<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 172  
taatccagca gtgcaggccg gg 22

<210> 173  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 173  
atggcctcca cggctgtgtg gaccgtgttc ctgggcaagg tgtggcagaa 50

<210> 174  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 174  
tgcctatgca ctgaggaggc agaag 25

<210> 175  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 175  
aggcaggac acagagtcca ttcac 25

<210> 176  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 176  
agtatgattt gccgtgcacc cagggccagt ggacgatcca gaacaggagg 50

<210> 177  
<211> 1510  
<212> DNA  
<213> Homo sapiens



<400> 177

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ctccagtccc ccagcccctg gccgagagaa ggggtcttacc ggccgggatt 150  
gctggaaaaca ccaagagggt gtttttggtt tttaaaactt ctgtttcttg 200  
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tgcagtttca acatgacagc taaaaccttt ttcatcattc acggatggac 500  
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caattgcata tggaacaatc acagagggtg taaaatgtga gcatgagcg 1050  
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tacctccttc ttaataccat gctgcagagc agggcacatc ctagcccagg 1350  
agaagtggcc agcacaatcc aatcaaatcg ttgcaaatca gattacactg 1400  
tgcatgtcct aggaagggga atctttacaa aataaacagt gtggaccct 1450

aataaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500

aaaaaaaaaa 1510

<210> 178

<211> 354

<212> PRT

<213> Homo sapiens

<400> 178

Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys Tyr  
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Cys Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg  
20 25 30

Leu Glu Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val  
35 40 45

Lys Pro Ser Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu  
50 55 60

His Glu Gly Cys Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu  
65 70 75

Asp Cys Ser Phe Asn Met Thr Ala Lys Thr Phe Phe Ile Ile His  
80 85 90

Gly Trp Thr Met Ser Gly Ile Phe Glu Asn Trp Leu His Lys Leu  
95 100 105

Val Ser Ala Leu His Thr Arg Glu Lys Asp Ala Asn Val Val Val  
110 115 120

Val Asp Trp Leu Pro Leu Ala His Gln Leu Tyr Thr Asp Ala Val  
125 130 135

Asn Asn Thr Arg Val Val Gly His Ser Ile Ala Arg Met Leu Asp  
140 145 150

Trp Leu Gln Glu Lys Asp Asp Phe Ser Leu Gly Asn Val His Leu  
155 160 165

Ile Gly Tyr Ser Leu Gly Ala His Val Ala Gly Tyr Ala Gly Asn  
170 175 180

Phe Val Lys Gly Thr Val Gly Arg Ile Thr Gly Leu Asp Pro Ala  
185 190 195

Gly Pro Met Phe Glu Gly Ala Asp Ile His Lys Arg Leu Ser Pro  
200 205 210

Asp Asp Ala Asp Phe Val Asp Val Leu His Thr Tyr Thr Arg Ser  
215 220 225

Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly His Ile Asp  
230 235 240

Footnote: The FOOT

Ile Tyr Pro Asn Gly Gly Asp Phe Gln Pro Gly Cys Gly Leu Asn	
245	250 255
Asp Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val Val	
260	265 270
Lys Cys Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu	
275	280 285
Val Asn Gln Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser	
290	295 300
Asn Arg Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg	
305	310 315
Cys Asn Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg	
320	325 330
Asn Ser Lys Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg	
335	340 345
Gly Asn Leu Gln Ser Leu Glu Cys Pro	
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<210> 179  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 179  
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<210> 180  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 180  
 gctattacaa cggttcttgc ggcagc 26

<210> 181  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 181  
 ttgactctct ggtgaatcag gacaagccga gttttgcctt ccag 44

<210> 182

<211> 3240  
<212> DNA  
<213> Homo sapiens

<400> 182  
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acgcgctgga ggagtggagc agcaccggc cggcctggg ggctgacagt 150  
cggcaaagtt tggcccgaag aggaagtggc ctcaaaccgc ggtaggtggc 200  
gaccaggcca gaccaggggc gctcgtgcc tgcgggcggg ctgtaggcga 250  
gggcgcgccc cagtgcgag acccggggct tcaggagccg gccccgggag 300  
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<212> PRT
<213> Homo sapiens
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Pro	Pro	Ala	Val	Leu	Leu	Glu	Val	Gln	Gly	Thr	Leu	Gln	Arg	Pro
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Leu	Val	Arg	Asp	Ser	Arg	Thr	Ser	Pro	Ala	Asn	Cys	Thr	Trp	Leu
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Ile	Leu	Gly	Ser	Lys	Glu	Gln	Thr	Val	Thr	Ile	Arg	Phe	Gln	Lys
				65					70					75
Leu	His	Leu	Ala	Cys	Gly	Ser	Glu	Arg	Leu	Thr	Leu	Arg	Ser	Pro
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Leu	Gln	Pro	Leu	Ile	Ser	Leu	Cys	Glu	Ala	Pro	Pro	Ser	Pro	Leu
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Gln	Leu	Pro	Gly	Gly	Asn	Val	Thr	Ile	Thr	Tyr	Ser	Tyr	Ala	Gly
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Ala	Arg	Ala	Pro	Met	Gly	Gln	Gly	Phe	Leu	Leu	Ser	Tyr	Ser	Gln
				125					130					135
Asp	Trp	Leu	Met	Cys	Leu	Gln	Glu	Glu	Phe	Gln	Cys	Leu	Asn	His
				140					145					150
Arg	Cys	Val	Ser	Ala	Val	Gln	Arg	Cys	Asp	Gly	Val	Asp	Ala	Cys
				155					160					165
Gly	Asp	Gly	Ser	Asp	Glu	Ala	Gly	Cys	Ser	Ser	Asp	Pro	Phe	Pro

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Gly Leu Thr Pro Arg Pro Val Pro Ser Leu Pro Cys Asn Val Thr	185		190		195
Leu Glu Asp Phe Tyr Gly Val Phe Ser Ser Pro Gly Tyr Thr His	200		205		210
Leu Ala Ser Val Ser His Pro Gln Ser Cys His Trp Leu Leu Asp	215		220		225
Pro His Asp Gly Arg Arg Leu Ala Val Arg Phe Thr Ala Leu Asp	230		235		240
Leu Gly Phe Gly Asp Ala Val His Val Tyr Asp Gly Pro Gly Pro	245		250		255
Pro Glu Ser Ser Arg Leu Leu Arg Ser Leu Thr His Phe Ser Asn	260		265		270
Gly Lys Ala Val Thr Val Glu Thr Leu Ser Gly Gln Ala Val Val	275		280		285
Ser Tyr His Thr Val Ala Trp Ser Asn Gly Arg Gly Phe Asn Ala	290		295		300
Thr Tyr His Val Arg Gly Tyr Cys Leu Pro Trp Asp Arg Pro Cys	305		310		315
Gly Leu Gly Ser Gly Leu Gly Ala Gly Glu Gly Leu Gly Glu Arg	320		325		330
Cys Tyr Ser Glu Ala Gln Arg Cys Asp Gly Ser Trp Asp Cys Ala	335		340		345
Asp Gly Thr Asp Glu Glu Asp Cys Pro Gly Cys Pro Pro Gly His	350		355		360
Phe Pro Cys Gly Ala Ala Gly Thr Ser Gly Ala Thr Ala Cys Tyr	365		370		375
Leu Pro Ala Asp Arg Cys Asn Tyr Gln Thr Phe Cys Ala Asp Gly	380		385		390
Ala Asp Glu Arg Arg Cys Arg His Cys Gln Pro Gly Asn Phe Arg	395		400		405
Cys Arg Asp Glu Lys Cys Val Tyr Glu Thr Trp Val Cys Asp Gly	410		415		420
Gln Pro Asp Cys Ala Asp Gly Ser Asp Glu Trp Asp Cys Ser Tyr	425		430		435
Val Leu Pro Arg Lys Val Ile Thr Ala Ala Val Ile Gly Ser Leu	440		445		450
Val Cys Gly Leu Leu Leu Val Ile Ala Leu Gly Cys Thr Cys Lys	455		460		465

Leu	Tyr	Ala	Ile	Arg	Thr	Gln	Glu	Tyr	Ser	Ile	Phe	Ala	Pro	Leu	470	475	480
Ser	Arg	Met	Glu	Ala	Glu	Ile	Val	Gln	Gln	Gln	Ala	Pro	Pro	Ser	485	490	495
Tyr	Gly	Gln	Leu	Ile	Ala	Gln	Gly	Ala	Ile	Pro	Pro	Val	Glu	Asp	500	505	510
Phe	Pro	Thr	Glu	Asn	Pro	Asn	Asp	Asn	Ser	Val	Leu	Gly	Asn	Leu	515	520	525
Arg	Ser	Leu	Leu	Gln	Ile	Leu	Arg	Gln	Asp	Met	Thr	Pro	Gly	Gly	530	535	540
Gly	Pro	Gly	Ala	Arg	Arg	Arg	Gln	Arg	Gly	Arg	Leu	Met	Arg	Arg	545	550	555
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Thr	Pro	Ala	Arg	Ala	Ser	Glu	Ala	Arg	Ser	Gln	Val	Thr	Pro	Ser	575	580	585
Ala	Ala	Pro	Leu	Glu	Ala	Leu	Asp	Gly	Gly	Thr	Gly	Pro	Ala	Arg	590	595	600
Glu	Gly	Gly	Ala	Val	Gly	Gly	Gln	Asp	Gly	Glu	Gln	Ala	Pro	Pro	605	610	615
Leu	Pro	Ile	Lys	Ala	Pro	Leu	Pro	Ser	Ala	Ser	Thr	Ser	Pro	Ala	620	625	630
Pro	Thr	Thr	Val	Pro	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Ser	Leu	Pro	635	640	645
Leu	Glu	Pro	Ser	Leu	Leu	Ser	Gly	Val	Val	Gln	Ala	Leu	Arg	Gly	650	655	660
Arg	Leu	Leu	Pro	Ser	Leu	Gly	Pro	Pro	Gly	Pro	Thr	Arg	Ser	Pro	665	670	675
Pro	Gly	Pro	His	Thr	Ala	Val	Leu	Ala	Leu	Glu	Asp	Glu	Asp	Asp	680	685	690
Val	Leu	Leu	Val	Pro	Leu	Ala	Glu	Pro	Gly	Val	Trp	Val	Ala	Glu	695	700	705
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<211> 20

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe



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 agaacatagg agcagtccca ctc 23  
  
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 tgcctgctgc tgcacaatct cag 23  
  
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 <210> 189  
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 <212> DNA  
 <213> Homo sapiens  
  
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 gaaagtgctg ctgctgggtc tgcagacgcg atggataacg tgcagccgaa 150



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<212> PRT  
<213> Homo sapiens

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20 25 30  
Thr Ser Met Thr Phe Phe Ile Ile Ala Gln Ala Pro Glu Pro Tyr  
35 40 45  
Ile Val Ile Thr Gly Phe Glu Val Thr Val Ile Leu Phe Phe Ile  
50 55 60  
Leu Leu Tyr Val Leu Arg Leu Asp Arg Leu Met Lys Trp Leu Phe  
65 70 75  
Trp Pro Leu Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe  
80 85 90  
Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr  
95 100 105  
Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys  
110 115 120  
Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn  
125 130 135  
Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu  
140 145 150



Val Leu

<210> 191  
<211> 495  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 78, 212, 234, 487  
<223> unknown base

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ggcactaact gngacatcta tgacctttt tatnatcgca caagcccctg 250  
aaccatatat tgttactact ggatttgaag tcaccgttat cttatttttc 300  
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gcctttgctt gatattatca actcactggt aacaacagta ttcatgctca 400  
tcgtatctgt gttggcactg ataccagaaa ccacaacatt gacagttggt 450  
ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 192  
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<210> 193  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 193  
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<210> 194  
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<212> DNA  
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<220>  
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<210> 195  
<211> 1879  
<212> DNA  
<213> Homo sapien

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 aaataattaa aaaaaaact tcattctaa 1879

<210> 196  
 <211> 518  
 <212> PRT  
 <213> Homo sapien

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 Leu Pro Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro  
 35 40 45  
 Thr Pro Gly Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu  
 50 55 60  
 Ala Leu Ala Leu Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala  
 65 70 75  
 Asn Phe Leu Ala Met Val Asp Asn Leu Gln Gly Asp Ser Gly Arg  
 80 85 90  
 Gly Tyr Tyr Leu Glu Met Leu Ile Gly Thr Pro Pro Gln Lys Leu  
 95 100 105





<210> 200  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

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<210> 201  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 201  
ggctctgtgc ctggatgg 18

<210> 202  
<211> 22  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 202  
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<210> 203  
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<220>  
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<220>  
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<210> 205  
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<213> Homo sapiens

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<210> 206  
 <211> 377  
 <212> PRT  
 <213> Homo sapiens

<400> 206  
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 35 40 45  
 Ser Gly Ile Gly Lys Met Thr Ala Leu Glu Leu Ala Arg Arg Gly  
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 Ala Arg Val Val Leu Ala Cys Arg Ser Gln Glu Arg Gly Glu Ala  
 65 70 75  
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 80 85 90  
 Phe Met Ala Leu Asp Leu Ala Ser Leu Ala Ser Val Arg Ala Phe  
 95 100 105  
 Ala Thr Ala Phe Leu Ser Ser Glu Pro Arg Leu Asp Ile Leu Ile  
 110 115 120  
 His Asn Ala Gly Ile Ser Ser Cys Gly Arg Thr Arg Glu Ala Phe  
 125 130 135  
 Asn Leu Leu Leu Arg Val Asn His Ile Gly Pro Phe Leu Leu Thr  
 140 145 150

His Leu Leu Leu Pro Cys Leu Lys Ala Cys Ala Pro Ser Arg Val  
 155 160 165  
 Val Val Val Ala Ser Ala Ala His Cys Arg Gly Arg Leu Asp Phe  
 170 175 180  
 Lys Arg Leu Asp Arg Pro Val Val Gly Trp Arg Gln Glu Leu Arg  
 185 190 195  
 Ala Tyr Ala Asp Thr Lys Leu Ala Asn Val Leu Phe Ala Arg Glu  
 200 205 210  
 Leu Ala Asn Gln Leu Glu Ala Thr Gly Val Thr Cys Tyr Ala Ala  
 215 220 225  
 His Pro Gly Pro Val Asn Ser Glu Leu Phe Leu Arg His Val Pro  
 230 235 240  
 Gly Trp Leu Arg Pro Leu Leu Arg Pro Leu Ala Trp Leu Val Leu  
 245 250 255  
 Arg Ala Pro Arg Gly Gly Ala Gln Thr Pro Leu Tyr Cys Ala Leu  
 260 265 270  
 Gln Glu Gly Ile Glu Pro Leu Ser Gly Arg Tyr Phe Ala Asn Cys  
 275 280 285  
 His Val Glu Glu Val Pro Pro Ala Ala Arg Asp Asp Arg Ala Ala  
 290 295 300  
 His Arg Leu Trp Glu Ala Ser Lys Arg Leu Ala Gly Leu Gly Pro  
 305 310 315  
 Gly Glu Asp Ala Glu Pro Asp Glu Asp Pro Gln Ser Glu Asp Ser  
 320 325 330  
 Glu Ala Pro Ser Ser Leu Ser Thr Pro His Pro Glu Glu Pro Thr  
 335 340 345  
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<210> 207

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

cttcattggcc ttggacttgg ccag 24

<210> 208  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 208  
acgccagtgg cctcaagctg gttg 24

<210> 209  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 209  
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<210> 210  
<211> 3716  
<212> DNA  
<213> Homo sapiens

<400> 210  
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caagcctcag gccagccacc tcccaccatc cgctgggtgc tgaatgggca 200  
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aaaaaaaaaa aaaaaa 3716

<210> 211

<211> 985

<212> PRT

<213> Homo sapiens

<400> 211

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Pro Gln Asp Gln Leu Phe Gln Gly Pro Gly Pro Ala Arg Met Ser  
20 25 30

Cys Gln Ala Ser Gly Gln Pro Pro Pro Thr Ile Arg Trp Leu Leu  
35 40 45

Asn Gly Gln Pro Leu Ser Met Val Pro Pro Asp Pro His His Leu  
50 55 60

Leu Pro Asp Gly Thr Leu Leu Leu Leu Gln Pro Pro Ala Arg Gly  
65 70 75

His Ala His Asp Gly Gln Ala Leu Ser Thr Asp Leu Gly Val Tyr  
80 85 90

Thr Cys Glu Ala Ser Asn Arg Leu Gly Thr Ala Val Ser Arg Gly  
95 100 105

Ala Arg Leu Ser Val Ala Val Leu Arg Glu Asp Phe Gln Ile Gln  
110 115 120

Pro Arg Asp Met Val Ala Val Val Gly Glu Gln Phe Thr Leu Glu  
125 130 135

Cys Gly Pro Pro Trp Gly His Pro Glu Pro Thr Val Ser Trp Trp  
140 145 150

Lys Asp Gly Lys Pro Leu Ala Leu Gln Pro Gly Arg His Thr Val  
155 160 165

Ser Gly Gly Ser Leu Leu Met Ala Arg Ala Glu Lys Ser Asp Glu  
170 175 180

Gly Thr Tyr Met Cys Val Ala Thr Asn Ser Ala Gly His Arg Glu  
185 190 195

Ser Arg Ala Ala Arg Val Ser Ile Gln Glu Pro Gln Asp Tyr Thr  
200 205 210

Glu Pro Val Glu Leu Leu Ala Val Arg Ile Gln Leu Glu Asn Val  
215 220 225

Thr Leu Leu Asn Pro Asp Pro Ala Glu Gly Pro Lys Pro Arg Pro  
230 235 240

TOH20T=H30ZT00T

Ala Val Trp Leu Ser Trp Lys Val Ser Gly Pro Ala Ala Pro Ala  
245 250 255

Gln Ser Tyr Thr Ala Leu Phe Arg Thr Gln Thr Ala Pro Gly Gly  
260 265 270

Gln Gly Ala Pro Trp Ala Glu Glu Leu Leu Ala Gly Trp Gln Ser  
275 280 285

Ala Glu Leu Gly Gly Leu His Trp Gly Gln Asp Tyr Glu Phe Lys  
290 295 300

Val Arg Pro Ser Ser Gly Arg Ala Arg Gly Pro Asp Ser Asn Val  
305 310 315

Leu Leu Leu Arg Leu Pro Glu Lys Val Pro Ser Ala Pro Pro Gln  
320 325 330

Glu Val Thr Leu Lys Pro Gly Asn Gly Thr Val Phe Val Ser Trp  
335 340 345

Val Pro Pro Pro Ala Glu Asn His Asn Gly Ile Ile Arg Gly Tyr  
350 355 360

Gln Val Trp Ser Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp  
365 370 375

Thr Val Val Gly Glu Gln Thr Gln Leu Glu Ile Ala Thr His Met  
380 385 390

Pro Gly Ser Tyr Cys Val Gln Val Ala Ala Val Thr Gly Ala Gly  
395 400 405

Ala Gly Glu Pro Ser Arg Pro Val Cys Leu Leu Leu Glu Gln Ala  
410 415 420

Met Glu Arg Ala Thr Gln Glu Pro Ser Glu His Gly Pro Trp Thr  
425 430 435

Leu Glu Gln Leu Arg Ala Thr Leu Lys Arg Pro Glu Val Ile Ala  
440 445 450

Thr Cys Gly Val Ala Leu Trp Leu Leu Leu Leu Gly Thr Ala Val  
455 460 465

Cys Ile His Arg Arg Arg Arg Ala Arg Val His Leu Gly Pro Gly  
470 475 480

Leu Tyr Arg Tyr Thr Ser Glu Asp Ala Ile Leu Lys His Arg Met  
485 490 495

Asp His Ser Asp Ser Gln Trp Leu Ala Asp Thr Trp Arg Ser Thr  
500 505 510

Ser Gly Ser Arg Asp Leu Ser Ser Ser Ser Ser Leu Ser Ser Arg  
515 520 525

Leu Gly Ala Asp Ala Arg Asp Pro Leu Asp Cys Arg Arg Ser Leu



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Leu Ser Trp Asp Ser Arg Ser Pro Gly	Val Pro Leu Leu Pro Asp	555
545	550	
Thr Ser Thr Phe Tyr Gly Ser Leu Ile	Ala Glu Leu Pro Ser Ser	570
560	565	
Thr Pro Ala Arg Pro Ser Pro Gln Val	Pro Ala Val Arg Arg Leu	585
575	580	
Pro Pro Gln Leu Ala Gln Leu Ser Ser	Pro Cys Ser Ser Ser Asp	600
590	595	
Ser Leu Cys Ser Arg Arg Gly Leu Ser	Ser Pro Arg Leu Ser Leu	615
605	610	
Ala Pro Ala Glu Ala Trp Lys Ala Lys	Lys Lys Gln Glu Leu Gln	630
620	625	
His Ala Asn Ser Ser Pro Leu Leu Arg	Gly Ser His Ser Leu Glu	645
635	640	
Leu Arg Ala Cys Glu Leu Gly Asn Arg	Gly Ser Lys Asn Leu Ser	660
650	655	
Gln Ser Pro Gly Ala Val Pro Gln Ala	Leu Val Ala Trp Arg Ala	675
665	670	
Leu Gly Pro Lys Leu Leu Ser Ser Ser	Asn Glu Leu Val Thr Arg	690
680	685	
His Leu Pro Pro Ala Pro Leu Phe Pro	His Glu Thr Pro Pro Thr	705
695	700	
Gln Ser Gln Gln Thr Gln Pro Pro Val	Ala Pro Gln Ala Pro Ser	720
710	715	
Ser Ile Leu Leu Pro Ala Ala Pro Ile	Pro Ile Leu Ser Pro Cys	735
725	730	
Ser Pro Pro Ser Pro Gln Ala Ser Ser	Leu Ser Gly Pro Ser Pro	750
740	745	
Ala Ser Ser Arg Leu Ser Ser Ser Ser	Leu Ser Ser Leu Gly Glu	765
755	760	
Asp Gln Asp Ser Val Leu Thr Pro Glu	Glu Val Ala Leu Cys Leu	780
770	775	
Glu Leu Ser Glu Gly Glu Glu Thr Pro	Arg Asn Ser Val Ser Pro	795
785	790	
Met Pro Arg Ala Pro Ser Pro Pro Thr	Thr Tyr Gly Tyr Ile Ser	810
800	805	
Val Pro Thr Ala Ser Glu Phe Thr Asp	Met Gly Arg Thr Gly Gly	825
815	820	

Gly Val Gly Pro Lys Gly Gly Val Leu Leu Cys Pro Pro Arg Pro  
830 835 840

Cys Leu Thr Pro Thr Pro Ser Glu Gly Ser Leu Ala Asn Gly Trp  
845 850 855

Gly Ser Ala Ser Glu Asp Asn Ala Ala Ser Ala Arg Ala Ser Leu  
860 865 870

Val Ser Ser Ser Asp Gly Ser Phe Leu Ala Asp Ala His Phe Ala  
875 880 885

Arg Ala Leu Ala Val Ala Val Asp Ser Phe Gly Phe Gly Leu Glu  
890 895 900

Pro Arg Glu Ala Asp Cys Val Phe Ile Asp Ala Ser Ser Pro Pro  
905 910 915

Ser Pro Arg Asp Glu Ile Phe Leu Thr Pro Asn Leu Ser Leu Pro  
920 925 930

Leu Trp Glu Trp Arg Pro Asp Trp Leu Glu Asp Met Glu Val Ser  
935 940 945

His Thr Gln Arg Leu Gly Arg Gly Met Pro Pro Trp Pro Pro Asp  
950 955 960

Ser Gln Ile Ser Ser Gln Arg Ser Gln Leu His Cys Arg Met Pro  
965 970 975

Lys Ala Gly Ala Ser Pro Val Asp Tyr Ser  
980 985

<210> 212  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 212  
gaaggacac acatgtgtgt ggcc 24

<210> 213  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 213  
actgacattc cagctgagcc acac 24

<210> 214  
<211> 50  
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 214

aggactacac ggagcctgtg gagcttctgg ctgtgcgaat tcagctggaa 50

<210> 215

<211> 2749

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 1869, 1887

<223> unknown base

<400> 215

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gcgggttcga aggggacact gtgtccctgc agtgaccta cagggaagag 150

ctgagggacc accggaagta ctggtgcagg aagggtggga tctctttctc 200

tcgtgtctct ggaccatct atgcagaaga agaaggccag gagacaatga 250

agggcagggt gtccatccgt gacagccgcc aggagctctc gtcattgtg 300

accctgtgga acctcaccct gcaagacgt ggggagtact ggtgtgggg 350

cgaaaaacgg ggccccgatg agtctttact gatctctctg ttctgtcttc 400

caggaccctg ctgtctctcc tccccttctc ccaccttcca gcctctggct 450

acaacacgcc tgcagcccaa ggcaaaagct cagcaaacc agccccagg 500

attgacttct cctgggtctt acccggcagc caccacagcc aagcagggga 550

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gaaaggactt ctcagtacac aggaacctct cctcaccag cgacctctcc 650

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104201 15041001

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<211> 332  
<212> PRT  
<213> Homo sapiens

<400> 216  
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Asp Thr Val Ser Leu Gln Cys Thr Tyr Arg Glu Glu Leu Arg Asp 45  
35 40  
His Arg Lys Tyr Trp Cys Arg Lys Gly Gly Ile Leu Phe Ser Arg 60  
50 55  
Cys Ser Gly Thr Ile Tyr Ala Glu Glu Glu Gly Gln Glu Thr Met 75  
65 70  
Lys Gly Arg Val Ser Ile Arg Asp Ser Arg Gln Glu Leu Ser Leu 90  
80 85  
Ile Val Thr Leu Trp Asn Leu Thr Leu Gln Asp Ala Gly Glu Tyr 105  
95 100  
Trp Cys Gly Val Glu Lys Arg Gly Pro Asp Glu Ser Leu Leu Ile 120  
110 115  
Ser Leu Phe Val Phe Pro Gly Pro Cys Cys Pro Pro Ser Pro Ser 135  
125 130  
Pro Thr Phe Gln Pro Leu Ala Thr Thr Arg Leu Gln Pro Lys Ala 150  
140 145  
Lys Ala Gln Gln Thr Gln Pro Pro Gly Leu Thr Ser Pro Gly Leu 165  
155 160  
Tyr Pro Ala Ala Thr Thr Ala Lys Gln Gly Lys Thr Gly Ala Glu 180  
170 175  
Ala Pro Pro Leu Pro Gly Thr Ser Gln Tyr Gly His Glu Arg Thr 195  
185 190  
Ser Gln Tyr Thr Gly Thr Ser Pro His Pro Ala Thr Ser Pro Pro

200	205	210
Ala Gly Ser Ser Arg Pro Pro Met Gln Leu Asp Ser Thr Ser Ala		
215	220	225
Glu Asp Thr Ser Pro Ala Leu Ser Ser Gly Ser Ser Lys Pro Arg		
230	235	240
Val Ser Ile Pro Met Val Arg Ile Leu Ala Pro Val Leu Val Leu		
245	250	255
Leu Ser Leu Leu Ser Ala Ala Gly Leu Ile Ala Phe Cys Ser His		
260	265	270
Leu Leu Leu Trp Arg Lys Glu Ala Gln Gln Ala Thr Glu Thr Gln		
275	280	285
Arg Asn Glu Lys Phe Trp Leu Ser Arg Leu Thr Ala Glu Glu Lys		
290	295	300
Glu Ala Pro Ser Gln Ala Pro Glu Gly Asp Val Ile Ser Met Pro		
305	310	315
Pro Leu His Thr Ser Glu Glu Glu Leu Gly Phe Ser Lys Phe Val		
320	325	330
Ser Ala		

<210> 217  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 217  
 ccctgcagtg cacctacagg gaag 24

<210> 218  
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 <212> DNA  
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<220>  
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<400> 218  
 ctgtcttccc ctgcttggt gtgg 24

<210> 219  
 <211> 47  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 219  
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<213> Homo sapiens

<400> 220  
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cagtgtgaaa gaaccagtgg tctcgctctg ttgccaggc tagagtgtac 150  
tggcgtgatc atagctcact gcagcctcag actcctggac ttgagaaatc 200  
ctcctgcctt agcctcctgc atatctggga ctccaggggt gcactcaagc 250  
cctgtttctt ctcttctgt gactggacca cggaggtctg tgagctgcct 300  
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ccgccggcat agaagccagg agcagggctc tcagaaggcg gtggtgccca 400  
gctgggatca tgttgttggc cctggtctgt ctgctcagct gcctgtacc 450  
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<212> PRT  
<213> Homo sapiens

<400> 221  
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 35 40 45  
 Trp Val Cys Leu Ala Tyr Phe Thr Ser Gly Phe Asn Ala Ala Ala  
 50 55 60  
 Leu Asp Tyr Glu Ala Asp Gly Ser Thr Asn Asn Gly Ile Phe Gln  
 65 70 75  
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 80 85 90  
 Asn Val Cys Arg Met Tyr Cys Ser Asp Leu Leu Asn Pro Asn Leu  
 95 100 105  
 Lys Asp Thr Val Ile Cys Ala Met Lys Ile Thr Gln Glu Pro Gln  
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<400> 224  
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<210> 225



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155



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Gln	Trp	Ser	Gly	Cys	Ser	Asp	Asn	Ile	Ala	Tyr	Gly	Val	Ala	Phe
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Ser	Gln	Ser	Phe	Val	Asp	Val	Arg	Glu	Arg	Ser	Lys	Gly	Ala	Ser
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Lys	Ala	Ile	Leu	Thr	His	Met	Arg	Val	Glu	Cys	Lys	Cys	His	Gly
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Pro	Phe	Arg	Gln	Val	Gly	His	Ala	Leu	Lys	Glu	Lys	Phe	Asp	Gly
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Ala	Thr	Glu	Val	Glu	Pro	Arg	Arg	Val	Gly	Ser	Ser	Arg	Ala	Leu
				245					250					255
Val	Pro	Arg	Asn	Ala	Gln	Phe	Lys	Pro	His	Thr	Asp	Glu	Asp	Leu
				260					265					270
Val	Tyr	Leu	Glu	Pro	Ser	Pro	Asp	Phe	Cys	Glu	Gln	Asp	Met	Arg
				275					280					285
Ser	Gly	Val	Leu	Gly	Thr	Arg	Gly	Arg	Thr	Cys	Asn	Lys	Thr	Ser
				290					295					300
Lys	Ala	Ile	Asp	Gly	Cys	Glu	Leu	Leu	Cys	Cys	Gly	Arg	Gly	Phe
				305					310					315
His	Thr	Ala	Gln	Val	Glu	Leu	Ala	Glu	Arg	Cys	Ser	Cys	Lys	Phe
				320					325					330
His	Trp	Cys	Cys	Phe	Val	Lys	Cys	Arg	Gln	Cys	Gln	Arg	Leu	Val
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				350										

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<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 227

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<220>  
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<210> 230  
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cgccatctgg gcaaggttca gggctaccag tgggtggacg gagtctctct 800  
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<210> 231  
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<213> Homo sapiens

<400> 231

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Pro	Leu	Phe	Leu	Ala	Leu	Ala	Val	Leu	Val	Thr	Thr	Val	Leu	Trp	35	40	45	
Ala	Val	Ile	Leu	Ser	Ile	Leu	Leu	Ser	Lys	Ala	Ser	Thr	Glu	Arg	50	55	60	
Ala	Ala	Leu	Leu	Asp	Gly	His	Asp	Leu	Leu	Arg	Thr	Asn	Ala	Ser	65	70	75	
Lys	Gln	Thr	Ala	Ala	Leu	Gly	Ala	Leu	Lys	Glu	Glu	Val	Gly	Asp	80	85	90	
Cys	His	Ser	Cys	Cys	Ser	Gly	Thr	Gln	Ala	Gln	Leu	Gln	Thr	Thr	95	100	105	
Arg	Ala	Glu	Leu	Gly	Glu	Ala	Gln	Ala	Lys	Leu	Met	Glu	Gln	Glu	110	115	120	
Ser	Ala	Leu	Arg	Glu	Leu	Arg	Glu	Arg	Val	Thr	Gln	Gly	Leu	Ala	125	130	135	





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tccctgataa	ctgcgtctaa	gaccagagcc	ccgcagcccc	tggggccccc	1300
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<213> Homo sapiens
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<400> 236

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20 25 30

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35 40 45

Thr Phe Thr Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr  
50 55 60

Pro Leu Phe Arg Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala  
65 70 75

Ala His Ser Ser Asp Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val  
80 85 90

Ser Asn Gly Leu Arg Asp Phe Ala Glu Arg Gly Glu Ala Trp Ala  
95 100 105

Leu Met Lys Glu Ile Glu Ala Ala Gly Glu Ala Leu Gln Ser Val





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 <400> 238  
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 <211> 24  
 <212> DNA  
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 <400> 242  
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				125					130					135	
Asp	Thr	Val	Tyr	Asn	Met	Leu	Arg	Leu	Ser	Glu	Val	Asp	Ile	Asp	
				140					145					150	
Asp	Asp	Glu	Arg	Pro	His	Asn	Pro	His	Lys	Ile	Lys	Ser	Cys	Glu	
				155					160					165	
Val	Leu	Phe	Asn	Pro	Phe	Asp	Asp	Ile	Ile	Pro	Arg	Glu	Ile	Lys	
				170					175					180	
Arg	Leu	Lys	Lys	Glu	Lys	Pro	Glu	Glu	Glu	Val	Lys	Lys	Leu	Lys	
				185					190					195	
Pro	Lys	Gly	Thr	Lys	Asn	Phe	Ser	Leu	Leu	Ser	Phe	Gly	Glu	Glu	
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Ala	Glu	Glu	Glu	Glu	Glu	Glu	Val	Asn	Arg	Val	Ser	Gln	Ser	Met	
				215					220					225	
Lys	Gly	Lys	Ser	Lys	Ser	Ser	His	Asp	Leu	Leu	Lys	Asp	Asp	Pro	
				230					235					240	
His	Leu	Ser	Ser	Val	Pro	Val	Val	Glu	Ser	Glu	Lys	Gly	Asp	Ala	
				245					250					255	
Pro	Asp	Leu	Val	Asp	Asp	Gly	Glu	Asp	Glu	Ser	Ala	Glu	His	Asp	
				260					265					270	
Glu	Tyr	Ile	Asp	Gly	Asp	Glu	Lys	Asn	Leu	Met	Arg	Glu	Arg	Ile	
				275					280					285	
Ala	Lys	Lys	Leu	Lys	Lys	Asp	Thr	Ser	Ala	Asn	Val	Lys	Ser	Ala	
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Gly	Glu	Gly	Glu	Val	Glu	Lys	Lys	Ser	Val	Ser	Arg	Ser	Glu	Glu	
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Leu	Arg	Lys	Glu	Ala	Arg	Gln	Leu	Lys	Arg	Glu	Leu	Leu	Ala	Ala	
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Lys	Gln	Lys	Lys	Val	Glu	Asn	Ala	Ala	Lys	Gln	Ala	Glu	Lys	Arg	
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Ser	Glu	Glu	Glu	Glu	Ala	Pro	Pro	Asp	Gly	Ala	Val	Ala	Glu	Tyr	
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Arg	Arg	Glu	Lys	Gln	Lys	Tyr	Glu	Ala	Leu	Arg	Lys	Gln	Gln	Ser	
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Lys	Lys	Gly	Thr	Ser	Arg	Glu	Asp	Gln	Thr	Leu	Ala	Leu	Leu	Asn	
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Gln	Phe	Lys	Ser	Lys	Leu	Thr	Gln	Ala	Ile	Ala	Glu	Thr	Pro	Glu	

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425	430	435
Ala Ser Met Gln Asp Ser Asp Thr Phe	Glu Ile Tyr Asp Pro Arg	
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470		

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<210> 247  
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<220>  
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 <400> 247  
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<210> 248  
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 <400> 248  
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<210> 249  
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 <212> PRT  
 <213> Homo sapiens

<400> 254

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Gly	Thr	Gly	Thr	Ser	Ser	Asn	Pro	Ser	Val	Gly	Leu	Asn	Phe	Gly
				35					40					45
Asn	Leu	Gly	Ser	Thr	Ser	Thr	Pro	Ala	Thr	Thr	Ser	Ala	Pro	Ser
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Ser	Gly	Phe	Gly	Thr	Gly	Leu	Phe	Gly	Ser	Lys	Pro	Ala	Thr	Gly
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Phe	Thr	Leu	Gly	Gly	Thr	Asn	Thr	Gly	Ala	Leu	His	Thr	Lys	Arg
				80					85					90
Pro	Gln	Val	Val	Thr	Lys	Tyr	Gly	Thr	Leu	Gln	Gly	Lys	Gln	Met
				95					100					105
His	Val	Gly	Lys	Thr	Pro	Ile	Gln	Val	Phe	Leu	Gly	Val	Pro	Phe
				110					115					120
Ser	Arg	Pro	Pro	Leu	Gly	Ile	Leu	Arg	Phe	Ala	Pro	Pro	Glu	Pro
				125					130					135





<210> 258  
<211> 2764  
<212> DNA  
<213> Homo sapiens

<400> 258  
gagaacaggc ctgtctcagg caggccctgc gcctcctatg cggagatgct 50  
actgccactg ctgtctgctt cgctgctggg cgggtcccag gctatggatg 100  
ggagattctg gatacagagt caggagtcag tgatggtgcc ggagggcctg 150  
tgcattctctg tgccttgctc tttctcctac ccccgacaag actggacagg 200  
gtctacccca gcttatggct actggttcaa agcagtgact gagacaacca 250  
aggggtgctcc tgtggccaca aaccaccaga gtcgagaggt ggaaatgagc 300  
acccggggcc gattccagct cactggggat cccgccaagg ggaactgctc 350  
cttggtgatc agagacgcgc agatgcagga tgagtcacag tacttctttc 400  
gggtggagag aggaagctat gtgacatata atttcatgaa cgatgggttc 450  
tttctaaaag taacagtgtc cagcttcacg cccagacccc aggaccacaa 500  
caccgacctc acctgccatg tggacttctc cagaaagggt gtgagcgcac 550  
agaggaccgt ccgactccgt gtggcctatg ccccagaga ccttgttatc 600  
agcatttcac gtgacaacac gccagccctg gagccccagc cccagggaaa 650  
tgtccatac ctggaagccc aaaaaggcca gttcctgcgg ctctctctgtg 700  
ctgtgacag ccagccccct gccacactga gctgggtcct gcagaacaga 750  
gtcctctcct cgtcccatcc ctggggccct agacccttg ggctggagct 800  
gcccggggtg aaggctgggg attcagggcg ctacacctgc cgagcggaga 850  
acaggcttgg ctcccagcag cgagccctgg acctctctgt gcagtatcct 900  
ccagagaacc tgagagtgat ggtttcccaa gcaaacagga cagtcttgga 950  
aaaccttggg aacggcacgt ctctcccagt actggagggc caaagcctgt 1000  
gcctggtctg tgtcacacac agcagcccc cagccaggct gagctggacc 1050  
cagaggggac aggttctgag cccctcccag ccctcagacc ccggggtcct 1100  
ggagctgcct cgggttcaag tgagacacga aggagagttc acctgccacg 1150  
ctcggcaccc actgggtcc cagcacgtct ctctcagcct ctccgtgcac 1200  
tataagaagg gactcatctc aacggcattc tccaacggag cgtttctggg 1250  
aatcggcatc acggtcttct ttttctctg cctggccctg atcatcatga 1300

agattctacc gaagagacgg actcagacag aaaccccgag gccaggttc 1350  
 tcccggcaca gcacgatcct ggattacatc aatgtggtcc cgacggctgg 1400  
 ccccttggtc cagaagcgga atcagaaagc cacaccaaac agtcctcgga 1450  
 cccctcctcc accaggtgct cctccccag aatcaaagaa gaaccagaaa 1500  
 aagcagtatc agttgcccag tttcccagaa cccaaatcat cactcaagc 1550  
 cccagaatcc caggagagcc aagaggagct ccattatgcc acgtcaact 1600  
 tcccaggcgt cagaccagg cctgaggccc ggatgccaa gggcaccag 1650  
 ggggattatg cagaagtcaa gttccaatga ggtctctta ggcttagga 1700  
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 cccagcactt tgggaggcta aggtgggtg attgcttgag cccaggagtt 2200  
 cgagaccagc ctgggcaaca tggtgaaacc ccattctctac aaaaaatata 2250  
 aaacatagct gggcttggtg gtgtgtgcct gtagtcccag ctgtcagaca 2300  
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 gccacgagag tgacctctgg tcgtcctcac tgctacactc ctgacagcac 2550  
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 agaaataacc ataaaagtgg gcaaccagca gctctaggcg ctgctcttgt 2700  
 ctatggagta gccattcttt tgttccttta ctttcttaat aaacttgctt 2750

tcaccttaaa aaaa 2764

<210> 259

<211> 544

<212> PRT

<213> Homo sapiens

<400> 259

Met Leu Leu Pro Leu Leu Leu Ser Ser Leu Leu Gly Gly Ser Gln  
1 5 10 15

Ala Met Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met  
20 25 30

Val Pro Glu Gly Leu Cys Ile Ser Val Pro Cys Ser Phe Ser Tyr  
35 40 45

Pro Arg Gln Asp Trp Thr Gly Ser Thr Pro Ala Tyr Gly Tyr Trp  
50 55 60

Phe Lys Ala Val Thr Glu Thr Thr Lys Gly Ala Pro Val Ala Thr  
65 70 75

Asn His Gln Ser Arg Glu Val Glu Met Ser Thr Arg Gly Arg Phe  
80 85 90

Gln Leu Thr Gly Asp Pro Ala Lys Gly Asn Cys Ser Leu Val Ile  
95 100 105

Arg Asp Ala Gln Met Gln Asp Glu Ser Gln Tyr Phe Phe Arg Val  
110 115 120

Glu Arg Gly Ser Tyr Val Thr Tyr Asn Phe Met Asn Asp Gly Phe  
125 130 135

Phe Leu Lys Val Thr Val Leu Ser Phe Thr Pro Arg Pro Gln Asp  
140 145 150

His Asn Thr Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys Gly  
155 160 165

Val Ser Ala Gln Arg Thr Val Arg Leu Arg Val Ala Tyr Ala Pro  
170 175 180

Arg Asp Leu Val Ile Ser Ile Ser Arg Asp Asn Thr Pro Ala Leu  
185 190 195

Glu Pro Gln Pro Gln Gly Asn Val Pro Tyr Leu Glu Ala Gln Lys  
200 205 210

Gly Gln Phe Leu Arg Leu Leu Cys Ala Ala Asp Ser Gln Pro Pro  
215 220 225

Ala Thr Leu Ser Trp Val Leu Gln Asn Arg Val Leu Ser Ser Ser  
230 235 240

His Pro Trp Gly Pro Arg Pro Leu Gly Leu Glu Leu Pro Gly Val  
245 250 255

TCACCTTA AAAA

Lys	Ala	Gly	Asp	Ser	Gly	Arg	Tyr	Thr	Cys	Arg	Ala	Glu	Asn	Arg	
				260					265					270	
Leu	Gly	Ser	Gln	Gln	Arg	Ala	Leu	Asp	Leu	Ser	Val	Gln	Tyr	Pro	
				275					280					285	
Pro	Glu	Asn	Leu	Arg	Val	Met	Val	Ser	Gln	Ala	Asn	Arg	Thr	Val	
				290					295					300	
Leu	Glu	Asn	Leu	Gly	Asn	Gly	Thr	Ser	Leu	Pro	Val	Leu	Glu	Gly	
				305					310					315	
Gln	Ser	Leu	Cys	Leu	Val	Cys	Val	Thr	His	Ser	Ser	Pro	Pro	Ala	
				320					325					330	
Arg	Leu	Ser	Trp	Thr	Gln	Arg	Gly	Gln	Val	Leu	Ser	Pro	Ser	Gln	
				335					340					345	
Pro	Ser	Asp	Pro	Gly	Val	Leu	Glu	Leu	Pro	Arg	Val	Gln	Val	Glu	
				350					355					360	
His	Glu	Gly	Glu	Phe	Thr	Cys	His	Ala	Arg	His	Pro	Leu	Gly	Ser	
				365					370					375	
Gln	His	Val	Ser	Leu	Ser	Leu	Ser	Val	His	Tyr	Lys	Lys	Gly	Leu	
				380					385					390	
Ile	Ser	Thr	Ala	Phe	Ser	Asn	Gly	Ala	Phe	Leu	Gly	Ile	Gly	Ile	
				395					400					405	
Thr	Ala	Leu	Leu	Phe	Leu	Cys	Leu	Ala	Leu	Ile	Ile	Met	Lys	Ile	
				410					415					420	
Leu	Pro	Lys	Arg	Arg	Thr	Gln	Thr	Glu	Thr	Pro	Arg	Pro	Arg	Phe	
				425					430					435	
Ser	Arg	His	Ser	Thr	Ile	Leu	Asp	Tyr	Ile	Asn	Val	Val	Pro	Thr	
				440					445					450	
Ala	Gly	Pro	Leu	Ala	Gln	Lys	Arg	Asn	Gln	Lys	Ala	Thr	Pro	Asn	
				455					460					465	
Ser	Pro	Arg	Thr	Pro	Pro	Pro	Pro	Gly	Ala	Pro	Ser	Pro	Glu	Ser	
				470					475					480	
Lys	Lys	Asn	Gln	Lys	Lys	Gln	Tyr	Gln	Leu	Pro	Ser	Phe	Pro	Glu	
				485					490					495	
Pro	Lys	Ser	Ser	Thr	Gln	Ala	Pro	Glu	Ser	Gln	Glu	Ser	Gln	Glu	
				500					505					510	
Glu	Leu	His	Tyr	Ala	Thr	Leu	Asn	Phe	Pro	Gly	Val	Arg	Pro	Arg	
				515					520					525	
Pro	Glu	Ala	Arg	Met	Pro	Lys	Gly	Thr	Gln	Ala	Asp	Tyr	Ala	Glu	
				530					535					540	
Val	Lys	Phe	Gln												

<210> 260  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 260  
caaagcctgc gcctggtctg tg 22

<210> 261  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 261  
ttctggagcc cagagggtgc tgag 24

<210> 262  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 262  
ggagctgccca cccattcaaa tggagcacga aggagagttc acctg 45

<210> 263  
<211> 2857  
<212> DNA  
<213> Homo sapiens

<400> 263  
tgaagagtaa tagttggaat caaaagagtc aacgcaatga actgttattt 50  
actgctgcgt tttatgttgg gaattcctct cctatggcct tgtcttggag 100  
caacagaaaa ctctcaaaca aagaaagtca agcagccagt gcgatctcat 150  
ttgagagtga agcgtggctg ggtgtggaac caattttttg taccagagga 200  
aatgaatacg actagtcac acatcggcca gctaagatct gatttagaca 250  
atggaaacaa ttctttccag tacaagcttt tgggagctgg agctggaagt 300  
acttttatca ttgatgaaag aacagggtgac atatatgcca tacagaagct 350  
tgatagagag gagcgatccc tctacatctt aagagcccag gtaatagaca 400  
tcgctactgg aagggtgtg gaacctgagt ctgagtttgt catcaaagtt 450





gaaaacagat tctatttcct gagaaaagtg aagatttcag agagaatata 1950  
 ttccaatatg atgatgaagg gggaggagaa gaagatacag aggcctttga 2000  
 tatagcagag ctgaggagta gtaccataat gcgggaacgc aagactcgga 2050  
 aaaccacaag cgctgagatc aggagcctat acaggcagtc tttgcaagtt 2100  
 ggccccgaca gtgccatatt caggaaattc attctggaaa agctcgaaga 2150  
 agctaatact gatccgtgtg cccctccttt tgattccctc cagacctacg 2200  
 cttttgaggg aacaggggtca ttagctggat cctgagctc cttagaatca 2250  
 gcagtctctg atcaggatga aagctatgat taccttaatg agttgggacc 2300  
 tcgctttaa agattagcat gcatgtttgg ttctgcagtg cagtcaaata 2350  
 attagggctt tttaccatca aaatttttaa aagtgcataat gtgtattcga 2400  
 acccaatggt agtcttaaag agttttgtgc cctggctcta tggcggggaa 2450  
 agccctagtc tatggagttt tctgatttcc ctggagtaaa tactccatgg 2500  
 ttattttaag ctacctacat gctgtcattg aacagagatg tggggagaaa 2550  
 tgtaaacaat cagctcacag gcatcaatac aaccagattt gaagtaaaat 2600  
 aatgtaggaa gatattaaaa gtagatgaga ggacacaaga tgtagtcgat 2650  
 ccttatgcga ttatattcatt atttacttag gaaagagtaa aaataccaaa 2700  
 cgagaaaatt taaaggagca aaaatttgca agtcaaataa aaatgtacaa 2750  
 atcgagataa catttacatt tctatcatat tgacatgaaa attgaaaatg 2800  
 tatagtcaga gaaattttca tgaattattc catgaagtat tgtttccttt 2850  
 atttaaa 2857

<210> 264

<211> 772

<212> PRT

<213> Homo sapiens

<400> 264

Met	Asn	Cys	Tyr	Leu	Leu	Leu	Arg	Phe	Met	Leu	Gly	Ile	Pro	Leu
1				5					10					15

Leu	Trp	Pro	Cys	Leu	Gly	Ala	Thr	Glu	Asn	Ser	Gln	Thr	Lys	Lys
				20					25					30

Val	Lys	Gln	Pro	Val	Arg	Ser	His	Leu	Arg	Val	Lys	Arg	Gly	Trp
				35					40					45

Val	Trp	Asn	Gln	Phe	Phe	Val	Pro	Glu	Glu	Met	Asn	Thr	Thr	Ser
				50					55					60

His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn		65	70	75
Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe		80	85	90
Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu		95	100	105
Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile		110	115	120
Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val		125	130	135
Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp		140	145	150
Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr		155	160	165
Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser		170	175	180
Gly	Asn	Asn	Ala	Arg	Leu	Leu	Tyr	Ser	Leu	Leu	Gln	Gly	Gln	Pro		185	190	195
Tyr	Phe	Ser	Val	Glu	Pro	Thr	Thr	Gly	Val	Ile	Arg	Ile	Ser	Ser		200	205	210
Lys	Met	Asp	Arg	Glu	Leu	Gln	Asp	Glu	Tyr	Trp	Val	Ile	Ile	Gln		215	220	225
Ala	Lys	Asp	Met	Ile	Gly	Gln	Pro	Gly	Ala	Leu	Ser	Gly	Thr	Thr		230	235	240
Ser	Val	Leu	Ile	Lys	Leu	Ser	Asp	Val	Asn	Asp	Asn	Lys	Pro	Ile		245	250	255
Phe	Lys	Glu	Ser	Leu	Tyr	Arg	Leu	Thr	Val	Ser	Glu	Ser	Ala	Pro		260	265	270
Thr	Gly	Thr	Ser	Ile	Gly	Thr	Ile	Met	Ala	Tyr	Asp	Asn	Asp	Ile		275	280	285
Gly	Glu	Asn	Ala	Glu	Met	Asp	Tyr	Ser	Ile	Glu	Glu	Asp	Asp	Ser		290	295	300
Gln	Thr	Phe	Asp	Ile	Ile	Thr	Asn	His	Glu	Thr	Gln	Glu	Gly	Ile		305	310	315
Val	Ile	Leu	Lys	Lys	Lys	Val	Asp	Phe	Glu	His	Gln	Asn	His	Tyr		320	325	330
Gly	Ile	Arg	Ala	Lys	Val	Lys	Asn	His	His	Val	Pro	Glu	Gln	Leu		335	340	345
Met	Lys	Tyr	His	Thr	Glu	Ala	Ser	Thr	Thr	Phe	Ile	Lys	Ile	Gln				

350	355	360
Val Glu Asp Val Asp Glu Pro Pro Leu Phe Leu Leu Pro Tyr Tyr		
365	370	375
Val Phe Glu Val Phe Glu Glu Thr Pro Gln Gly Ser Phe Val Gly		
380	385	390
Val Val Ser Ala Thr Asp Pro Asp Asn Arg Lys Ser Pro Ile Arg		
395	400	405
Tyr Ser Ile Thr Arg Ser Lys Val Phe Asn Ile Asn Asp Asn Gly		
410	415	420
Thr Ile Thr Thr Ser Asn Ser Leu Asp Arg Glu Ile Ser Ala Trp		
425	430	435
Tyr Asn Leu Ser Ile Thr Ala Thr Glu Lys Tyr Asn Ile Glu Gln		
440	445	450
Ile Ser Ser Ile Pro Leu Tyr Val Gln Val Leu Asn Ile Asn Asp		
455	460	465
His Ala Pro Glu Phe Ser Gln Tyr Tyr Glu Thr Tyr Val Cys Glu		
470	475	480
Asn Ala Gly Ser Gly Gln Val Ile Gln Thr Ile Ser Ala Val Asp		
485	490	495
Arg Asp Glu Ser Ile Glu Glu His His Phe Tyr Phe Asn Leu Ser		
500	505	510
Val Glu Asp Thr Asn Asn Ser Ser Phe Thr Ile Ile Asp Asn Gln		
515	520	525
Asp Asn Thr Ala Val Ile Leu Thr Asn Arg Thr Gly Phe Asn Leu		
530	535	540
Gln Glu Glu Pro Val Phe Tyr Ile Ser Ile Leu Ile Ala Asp Asn		
545	550	555
Gly Ile Pro Ser Leu Thr Ser Thr Asn Thr Leu Thr Ile His Val		
560	565	570
Cys Asp Cys Gly Asp Ser Gly Ser Thr Gln Thr Cys Gln Tyr Gln		
575	580	585
Glu Leu Val Leu Ser Met Gly Phe Lys Thr Glu Val Ile Ile Ala		
590	595	600
Ile Leu Ile Cys Ile Met Ile Ile Phe Gly Phe Ile Phe Leu Thr		
605	610	615
Leu Gly Leu Lys Gln Arg Arg Lys Gln Ile Leu Phe Pro Glu Lys		
620	625	630
Ser Glu Asp Phe Arg Glu Asn Ile Phe Gln Tyr Asp Asp Glu Gly		
635	640	645

Gly Gly Glu Glu Asp Thr Glu Ala Phe Asp Ile Ala Glu Leu Arg  
650 655 660

Ser Ser Thr Ile Met Arg Glu Arg Lys Thr Arg Lys Thr Thr Ser  
665 670 675

Ala Glu Ile Arg Ser Leu Tyr Arg Gln Ser Leu Gln Val Gly Pro  
680 685 690

Asp Ser Ala Ile Phe Arg Lys Phe Ile Leu Glu Lys Leu Glu Glu  
695 700 705

Ala Asn Thr Asp Pro Cys Ala Pro Pro Phe Asp Ser Leu Gln Thr  
710 715 720

Tyr Ala Phe Glu Gly Thr Gly Ser Leu Ala Gly Ser Leu Ser Ser  
725 730 735

Leu Glu Ser Ala Val Ser Asp Gln Asp Glu Ser Tyr Asp Tyr Leu  
740 745 750

Asn Glu Leu Gly Pro Arg Phe Lys Arg Leu Ala Cys Met Phe Gly  
755 760 765

Ser Ala Val Gln Ser Asn Asn  
770

<210> 265

<211> 349

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 24, 60, 141, 226, 228, 249, 252

<223> unknown base

<400> 265

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gaatattttt taaaatggat agagaactgc aagatgagta ttgggtaatc 100

attcaagcca aggacatgat tggtcagcca ggagcgttgt ntggaacaac 150

aagtgtatta attaaacttt cagatgttaa tgacaataag cctatattta 200

aagaaagttt ataccgcttg actgtntntg aatctgcacc cactgggant 250

tntataggaa caatcatggc atatgataat gacataggag agaattgcaga 300

aatggattac agcattgaag aggatgattc gcaaacattt gacattatt 349

<210> 266

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 266  
cttgactgtc tctgaatctg caccc 25

<210> 267

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 267  
aagtgggtgga agcctccagt gtgg 24

<210> 268

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 268  
ccactacggt attagagcaa aagttaaaaa ccatcatggt tcctggagca 50  
gc 52

<210> 269

<211> 2747

<212> DNA

<213> Homo sapiens

<400> 269  
gcaacctcag cttctagtat ccagactcca gcgccgcccc gggcgaggac 50  
cccaaccccc acccagagct tctccagcgg cggcgcagcg agcagggctc 100  
cccgcccttaa cttcctccgc ggggccccagc caccttcggg agtccgggtt 150  
gcccacctgc aaactctccg ctttctgcac ctgccacccc tgagccagcg 200  
cgggcccccg agcgagtcac ggccaacgcg gggctgcagc tgttgggctt 250  
cattctcgcc ttcttgaggat ggatcggcgc catcgtcagc actgccctgc 300  
cccagtgagc gatttactcc tatgccggcg acaacatcgt gaccgcccag 350  
gccatgtacg aggggctgtg gatgtcctgc gtgtcgcaga gcaccgggca 400  
gatccagtgc aaagtctttg actccttgct gaatctgagc agcacattgc 450  
aagcaaccgc tgccttgatg gtggttgcca tcctcctggg agtgatagca 500  
atctttgtgg ccaccgttg catgaagtgt atgaagtgt tggaagacga 550  
tgagggtcag aagatgagga tggctgtcat tgggggtgcg atatttcttc 600



tttatattac tcttattctt tgaacatgaa ctatgcctat gtagtgtctt 2100  
 tatttgctca gctggctgag aactgaaga agtcactgaa caaacctac 2150  
 acacgtacct tcattgtgatt cactgccttc ctctctctac cagtctattt 2200  
 ccactgaaca aaacctacac acataccttc atgtggttca gtgccttcct 2250  
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 gtgtctgaca tgtttggtct ctgttccatt ttaacaactg ctcttacttt 2400  
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 aggggtgttg cactggtgtc tggagacctg gatttgagtc ttggtgctat 2500  
 caatcaccgt ctgtgtttga gcaaggcatt tggctgctgt aagcttattg 2550  
 cttcatctgt aagcgggtgt ttgtaattcc tgatcttccc acctcacagt 2600  
 gatgttggtg ggatccagtg agatagaata catgtaagtg tggttttgta 2650  
 atttaaaaag tgctatacta agggaaagaa ttgaggaatt aactgcatac 2700  
 gttttggtgt tgcttttcaa atgtttgaaa ataaaaaaaa tgtaag 2747

<210> 270

<211> 211

<212> PRT

<213> Homo sapiens

<400> 270

Met	Ala	Asn	Ala	Gly	Leu	Gln	Leu	Leu	Gly	Phe	Ile	Leu	Ala	Phe
1				5					10					15
Leu	Gly	Trp	Ile	Gly	Ala	Ile	Val	Ser	Thr	Ala	Leu	Pro	Gln	Trp
				20					25					30
Arg	Ile	Tyr	Ser	Tyr	Ala	Gly	Asp	Asn	Ile	Val	Thr	Ala	Gln	Ala
				35					40					45
Met	Tyr	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Ser	Gln	Ser	Thr	Gly
				50					55					60
Gln	Ile	Gln	Cys	Lys	Val	Phe	Asp	Ser	Leu	Leu	Asn	Leu	Ser	Ser
				65					70					75
Thr	Leu	Gln	Ala	Thr	Arg	Ala	Leu	Met	Val	Val	Gly	Ile	Leu	Leu
				80					85					90
Gly	Val	Ile	Ala	Ile	Phe	Val	Ala	Thr	Val	Gly	Met	Lys	Cys	Met
				95					100					105
Lys	Cys	Leu	Glu	Asp	Asp	Glu	Val	Gln	Lys	Met	Arg	Met	Ala	Val
				110					115					120



Ile Gly Gly Ala	Ile Phe Leu Leu Ala	Gly Leu Ala Ile Leu Val
125		130 135
Ala Thr Ala Trp Tyr Gly Asn Arg Ile Val Gln Glu Phe Tyr Asp		
140		145 150
Pro Met Thr Pro Val Asn Ala Arg Tyr Glu Phe Gly Gln Ala Leu		
155		160 165
Phe Thr Gly Trp Ala Ala Ala Ser Leu Cys Leu Leu Gly Gly Ala		
170		175 180
Leu Leu Cys Cys Ser Cys Pro Arg Lys Thr Thr Ser Tyr Pro Thr		
185		190 195
Pro Arg Pro Tyr Pro Lys Pro Ala Pro Ser Ser Gly Lys Asp Tyr		
200		205 210

Val

<210> 271  
 <211> 564  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 21, 69, 163, 434, 436, 444  
 <223> unknown base

<400> 271  
 ttctggccaa acccggggct ncagctgttg ggcttcatct cgccttcctg 50  
 ggatggatcg ggcctatcnt cacactgccc ttccccagtg gaggatttta 100  
 ctccctatgc tggcgacaac atcgtgaccg cccagcccat gtacgagggg 150  
 ctgtggatgt ccngcgtgtc gcagagcacc gggcagatcc agtgcaaagt 200  
 ctttgactcc ttgtgaate tgagcagcac attgcaagca acccgtgcct 250  
 tgatggtggt tggcatcctc ctgggagtga tagcaatctt tgtggccacc 300  
 gttggcatga agtgtatgaa gtgcttgaa gacgatgagg tgcagaagat 350  
 gaggatggct gtcattggg ggcgataatt tcttcttgca ggtctggcta 400  
 ttttagttgc cacagcatgg tatggcaata gaancnttca acanttctat 450  
 gaccctatga cccagtcaa tgccaggtac gaatttggtc aggtctcttt 500  
 cactggctgg gctgctgctt ctctctgcct tctgggaggt gccctacttt 550  
 gctgttctctg tccc 564

<210> 272  
 <211> 498

<212> DNA  
<213> Homo sapiens

<220>

<221> unsure

<222> 30, 49, 102, 141, 147, 171, 324-325, 339-341

<223> unknown base

<400> 272

acccttgacc caacgcggcc ccccgaccgn ttcatggcca aacgcgggnc 50  
tccagctggt gggcttcatt ctccccttcc tgggatggac cggcgcccat 100  
cntcagcact gccctgcccc agtggaggat ttactcctat nccgcnaca 150  
acatcgtgac cgcccaggcc ntgtacgagg ggctgtggat gtcctgcgtg 200  
tcgcagagca ccgggcagat ccagtgc aaa gtctttgact cccttgctga 250  
atctgagcag cacattgcaa gcaaccctg ccttgatggt ggttggcatc 300  
ctcctgggag tgatagcaat cttnttggcc accgttgttn ntgaagtgt 350  
tgaagtgtt ggaagacgat gaggtgcaga agatgaggat ggctgtcatt 400  
gggggcgcga tatttcttct tgcaggtctg gctatttttag ttgccacagc 450  
atggtatggc aatagaatcg ttcaagaatt ctatgacct atgaccga 498

<210> 273

<211> 552

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394

<223> unknown base

<400> 273

gggcccgacc attatccaac cgggntcact gttggtcat ctccctctg 50  
gatgaancgc gccatcntca gactccctgc cccatggaga tttncctat 100  
gctggcgaca acatcntgac cccagccat gtacgagggg ctttgaacgt 150  
cngcgtgtcg cagancaccg ggcagatcca gtgcaaagtc tttgactcct 200  
tgctgaatct gngcagcaca ttgcagcaac ccntgccctg atggtggtt 250  
gcatectcct gggagtgata gcaatctttg tggccaccgt tggcatgaag 300  
tgtatgaagt gcttgaaga cgatgaggtg cagaagatga ggatggctgt 350  
cattgggggc gcgatatttc ttcttgagg tctggctatt tnnngttgcc 400  
acagcatggt atggcaatag aatcgttcaa gaattctatg accctatgac 450

cccagtc aat gccaggtacg aatttgggtca ggctctcttc actgggtggg 500  
 ctgctgcttc tctctgcctt ctgggagggtg ccctactttg ctgttcctgc 550  
 ga 552

<210> 274  
 <211> 526  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407  
 <223> unknown base

<400> 274  
 attctcccct cctggatgga tcgcncacc gtcacattgc cttccccan 50

tgaggattn actcctatgc tggcgacaac atcgtgaccc cccaggccat 100  
 ttaccgaggg gctttggatg tcntgcntgt cgcagagcac cgggcagatc 150  
 ccagtgc aaa gtctttgact ccttgctgaa tctgagcagc acattgcaag 200  
 caaccctgct cttgatgggg ttggcatcct cctgggagtg atagcaacct 250  
 ttgtggccac cgttggcatg aagtgtatga agtgcttga agacgatgag 300  
 gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttcttgttg 350  
 caggctctggc tattttagtn gccacagcat ggtatggcaa tagantnntt 400  
 cnnnnntct atgaccctat gacccagtc aatgccaggt acgaatttgg 450  
 tcaggctctc ttcactggct gggctgctgc ttctctctgc cttctgggag 500  
 gtgccctact ttgctgttcc tgtccc 526

<210> 275  
 <211> 398  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274  
 <223> unknown base

<400> 275  
 agagcaccgg cagatcccag tncaaagtct ttgacccttg ctgaatctga 50  
 gcagcacatt ncaagcaacc ccttgcccttg aagggtggtg ncatcccccc 100  
 tgggagtga tagcaatctt tgtggccacc gttggcatga agtntatgaa 150  
 gtgcttgga gacgatgagg tgcagaagat gaggatggct gtcattgggg 200

gcgcgatatt tcttcttgca ggtctggcta ttttagtnnc cacagcatgg 250  
 tatggcaata gnatnnttcg nggnttctat gaccctatga cccagtcaa 300  
 tgccaggtagc gaatttggtc aggctctctt cactggctgg gctgctgctt 350  
 ctctctgcct tctgggaggt gccctacttt gctgttcctg tccccgaa 398

<210> 276  
 <211> 495  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476  
 <223> unknown base

<400> 276  
 agcaatgccc tgccccagc ggaggattaa ttcctatgnt ggggacaaca 50  
 ttgtgacngc ccaggccatg tacggggggc tgtggatgtc ctgctgtctg 100  
 cagagcaccg ggcagatcca gtgcaaagtn tttgactcct tgctgaattt 150  
 gagcagcaca ttgcaagcaa cccgtgcctt gatggtggtt ggcatcttcc 200  
 tgggagtgat agcaatcttt gtggccaccg tggnaatgaa gtgtatgaag 250  
 tgcttggaag acgatgaggt gcagaagatg aggatggctg tcattggggg 300  
 cgcgatattt ctntttgcag gtctggctat tttagttgcc acagcatggt 350  
 atggcaatag aatngttcaa gaattttatg accctatgac cccagtcaat 400  
 gccaggtagc aatttggtca ggctttnttc actggctggg ctgctgcttn 450  
 tttctgcctt ntgggaggtg ccctantttg ctgttcctgc gaacc 495

<210> 277  
 <211> 200  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 34, 87, 138, 147, 163, 165-166, 172  
 <223> unknown base

<400> 277  
 tcataggggg gcgcgatatt ttttcttgca ggtntggtta ttttagttgc 50  
 cacagcatgg tatggcaata gaatcgttca agaattntat gaccctatga 100  
 cccagtcaa tgccaggtagc gaatttggtc aggctctntt cactggntgg 150  
 gctgctgctt ctntnngcct tntgggaggt gccctacttt gctgttcctg 200

<210> 278  
<211> 542  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 26, 43, 55, 77, 198, 361-362, 391-392, 396  
<223> unknown base

<400> 278  
ttcctgggat ggatccgccc ccatactcac atgccctgcc ccttgagat 50  
ttacnccat gctggcgaac aacatctga ccgccaggc catgtacgag 100  
gggctgtgga atgtcctgcg tgtcccagag caccgggcag atccagtgc 150  
aagtctttga ctcccttgctg aatctgagca gcacattgca agcaaccntg 200  
ccttgatggt ggttggcatc ctccctgggag tgatagcaat ctttgtggcc 250  
accgttggca tgaaagtga tgaagtgtt ggaagacgat gaggtgcaga 300  
agatgaggat ggctgtcatt gggggcgca tatttcttct tgcaggtctg 350  
gctattttag nngccacagc atggtatggc aatcagaccc nntcanaaac 400  
tctatgacc tatgaccca gtcaatgcca ggtacgaatt tggtcaggct 450  
ctcttcaact gctgggctgc tgcttctctc tgccttcttg gaggtgccct 500  
actttgctgt tctgtcccc gaaaaacaac ctcttacca cg 542

<210> 279  
<211> 548  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 90, 115, 147, 228, 387  
<223> unknown base

<400> 279  
cggggctgca gctgttgggc ttcatctcgc ttccctgggat ggaatcggcg 50  
ccatcgtcag cactgccctg ccccatggag gatttactcn tatgtggcg 100  
acaacatcgt gaccncccag gccatgtacg aggggctgtg gatgtcngcg 150  
tgtcgcagag caccgggcag atccagtgc aagtctttga ctcccttgctg 200  
aatctgagca gcacattgca agcaaccntg ccttgatggt ggttggcatc 250  
ctccctgggag tgatagcaat ctttgtggcc accgttggca tgaagtgtat 300  
gaagtgttg gaagacgatg aggtgcagaa gatgaggatg gctgtcattg 350

ggggcgcgat atttcttctt gcaggctctgg ctatttntag ttgccacagc 400  
 atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccccag 450  
 tcaatgccag gtacgaattt ggtcaggctc tcttcactgg ctgggctgct 500  
 gcttctctct gccttctggg aggtgcccta ctttgctgtt cctgcgaa 548

<210> 280  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 280  
 cgagcgagtc atggccaacg c 21

<210> 281  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 281  
 gtgtcacacg tagtctttcc cgctgg 26

<210> 282  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 282  
 ctgcagctgt tgggcttcat tctgccttc ctgggatgga tcg 43

<210> 283  
 <211> 2285  
 <212> DNA  
 <213> Homo sapiens

<400> 283  
 gcgtgccgtc agctcgccgg gcaccgcggc ctgcgcctcg cctccgccc 50  
 ctgcgcctgc accgcgtaga ccgaccccc cctccagcgc gccacccgg 100  
 tagaggaccc ccgcccgtgc cccgaccggt cccgccttt ttgtaaaact 150  
 taaagcgggc gcagcattaa cgcttcccgc cccggtgacc tctcaggggt 200  
 ctccccgcca aaggtgctcc gccgctaagg aacatggcga aggtggagca 250  
 ggtcctgagc ctgcagccgc agcacgagct caaattccga ggtcccttca 300







Pro	Ile	Val	Ser	Lys	Ser	Leu	Ser	Ser	Ser	Leu	Asp	Asp	Thr	Glu
				155					160					165
Val	Lys	Lys	Val	Met	Glu	Glu	Cys	Lys	Arg	Leu	Gln	Gly	Glu	Val
				170					175					180
Gln	Arg	Leu	Arg	Glu	Glu	Asn	Lys	Gln	Phe	Lys	Glu	Glu	Asp	Gly
				185					190					195
Leu	Arg	Met	Arg	Lys	Thr	Val	Gln	Ser	Asn	Ser	Pro	Ile	Ser	Ala
				200					205					210
Leu	Ala	Pro	Thr	Gly	Lys	Glu	Glu	Gly	Leu	Ser	Thr	Arg	Leu	Leu
				215					220					225
Ala	Leu	Val	Val	Leu	Phe	Phe	Ile	Val	Gly	Val	Ile	Ile	Gly	Lys
				230					235					240

Ile Ala Leu

Footnote 130

<210> 285  
 <211> 418  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 40, 53, 68, 119, 134, 177-178, 255  
 <223> unknown base

<400> 285  
 gtcagtcttc tagattgtcc ttatcccacc ttccaaccan tactcacatt 50  
 tcnagcgccc aggtccangt ctgagcctga ctcccccttg gggacctagc 100  
 ctggagtcag gacaatggnt cgggctgcag agnnttagaa gcgagggcac 150  
 cagcagtttt ggggtggggag caagggnnga gagaaactct tcagcgaatc 200  
 cttctagtag tagttgagag tttgactgtg aattaatttt atgccataaa 250  
 agacnaaccc agttctgttt gactatgtag catcttgaaa agaaaaatta 300  
 taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350  
 ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400  
 gttaacttta aaatgagc 418

<210> 286  
 <211> 543  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 73, 97

<223> unknown base  
 <400> 286  
 tattgtaaag gccattttaa accattggta ggccttggt catgatgctg 50  
 gattacctcc ttaaatagaca ccnttcctcg cctgttggtg ctggccnttg 100  
 gggagctgga gccccagcat gctggggagt gcggtcagct ccacacagta 150  
 gtccccacgt ggcccactcc cggcccaggc tgctttccgt gtcttcagtt 200  
 ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagccca 250  
 aaggaattgc cactgtggca gcatcagacg tactcgatcat aagtgaagg 300  
 cgtgtgttga ctgattgacc cagcgctttg gaaataaatg gcagtgcctt 350  
 gttcacttaa agggaccaag ctaaattgta ttggttcag tagtgaagtc 400  
 aaactgttat tcagagatgt ttaatgcata ttaacttat ttaatgtatt 450  
 tcatctcatg ttttcttatt gtcacaagag tacagttaat gctgcgtgct 500  
 gctgaactct gttgggtgaa ctggtattgc tgctggaggg ctg 543  
 <210> 287  
 <211> 270  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> unsure  
 <222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242  
 <223> unknown base  
 <400> 287  
 ccctgggtggt tttgttcttt aattcggttg tgtaattntt gggaagattg 50  
 cttgtagagg tagnatgcac cnggctggta aattggattg gtggatccac 100  
 catatccatg ggatttaaat ttatcataac catgtgtaaa aagaaattaa 150  
 tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200  
 acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250  
 agttaaaaaat gtatagtaac 270  
 <210> 288  
 <211> 428  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> unsure  
 <222> 35, 116, 129, 197, 278, 294, 297, 349, 351  
 <223> unknown base

<400> 288  
 ggtggcccat tcccggccca ggctgctttc cggtnntcag ttctgtccaa 50  
 gccatcagct ccttgggact gatgaacaga gtcagaagcc caaaggaatt 100  
 gcactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150  
 actgattgac ccagcgcttt ggaaataaat ggcagtgttt tggtcantta 200  
 aagggaccaa gctaaatttg tattggttca tgtagtgaag tcaaactgtt 250  
 attcagagat gtttaatgca tatttaantt atttaagtta tttnatntca 300  
 tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350  
 ntgttgggtg aactgggtatt gctgctggag ggctgtgggc tcctctgtct 400  
 ttggagagtc-tggatcatgtg gaggtggg 428

<210> 289  
 <211> 320  
 <212> DNA  
 <213> Homo sapiens

<400> 289  
 tgctttccgt gtcttcagtt ctgtccaagc catcagctcc ttgggacttg 50  
 atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagacg 100  
 tactcgtcat aagtgaagagg cgtgtgttga ctgattgacc cagcgctttg 150  
 gaaataaatg gcagtgtttt gttcacttaa agggaccaag ctaaatttgt 200  
 attggttcat gtagtgaagt caaactgtta ttcagagatg tttaatgcat 250  
 atttaactta tttaatgtat ttcattctcat gttttcttat tgtcacaaga 300  
 gtacagttaa tgctgcgtgc 320

<210> 290  
 <211> 609  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,  
 447, 481, 513, 532, 584, 598  
 <223> unknown base

<400> 290  
 aaacctttaa aagttgaggg gaaaagaatg atcctttatt aatgacaagg 50  
 gaaacntgn gtaatccac aatggcatat tgtaaatgtc attttaaaca 100  
 ttggtaggcc ttggtacatg atgctggatt acctctctta aaatgacacc 150  
 cttcctcgcc tgttgggtgt ggcccttggg gagctngagc ccagcatgct 200



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

aaccaccaga gccaagagcc ggg 23

<210> 294

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cagcggaaatc atcgatgcag gggcctcaat taatgtatct gtgatgttac 50

<210> 295

<211> 2530

<212> DNA

<213> Homo sapiens

<400> 295

gcgagctccg ggtgctgtgg cccggccttg gcggggcggc ctccggctca 50

ggctggctga gaggtccca gctgcagcgt cccgccccgc ctctcgga 100

gctctgatct cagctgacag tgccctcggg gaccaaacia gcctggcagg 150

gtctcacttt gttgcccagg ctggagttca gtgcatgat catggtttac 200

tgcagccttg acctctggg ttcaagcgat cctgctgagt agctgggact 250

acaggacaaa attagaagat caaaatggaa aatatgctgc ttgggttgat 300

atttttcacc cctgggtgga ccctcattga tggatctgaa atggaatggg 350

attttatgtg gcacttgaga aaggtacccc ggattgtcag tgaaaggact 400

ttccatctca ccagccccgc atttgaggca gatgctaaga tgatggtaaa 450

tacagtgtgt ggcacgaat gccagaaaga actcccaact cccagccttt 500

ctgaattgga ggattatctt tcctatgaga ctgtctttga gaatggcacc 550

cgaaccttaa ccagggtgaa agttcaagat ttggttcttg agccgactca 600

aaatatcacc acaaaggag tatctgtag gagaaagaga caggtgtatg 650

gcaccgacag caggttcagc atcttggaca aaaggttctt aaccaatttc 700

cctttcagca cagctgtgaa gctttccacg ggctgtagtg gcattctcat 750

ttcccctcag catgttctaa ctgctgccca ctgtgttcat gatggaaagg 800

actatgtcaa agggagttaa aagctaagg tagggttgtt gaagatgagg 850



cttcacaaat tatgaatgat catgtgttga aagccacatt attttatgct 2350  
 atacattcta tgtatgaggt gctacatttt taggacaaag aattctgtaa 2400  
 tctttttcaa gaaagagtct ttttctcctt gacaaaatcc agcttttgta 2450  
 tgaggactat agggatgaatt ctctgattag taattttaga tatgtccttt 2500  
 cctaaaaatg aataaaattt atgaatatga 2530

<210> 296  
 <211> 413  
 <212> PRT  
 <213> Homo sapiens

<400> 296

Met	Glu	Asn	Met	Leu	Leu	Trp	Leu	Ile	Phe	Phe	Thr	Pro	Gly	Trp
1				5					10					15
Thr	Leu	Ile	Asp	Gly	Ser	Glu	Met	Glu	Trp	Asp	Phe	Met	Trp	His
				20					25					30
Leu	Arg	Lys	Val	Pro	Arg	Ile	Val	Ser	Glu	Arg	Thr	Phe	His	Leu
				35					40					45
Thr	Ser	Pro	Ala	Phe	Glu	Ala	Asp	Ala	Lys	Met	Met	Val	Asn	Thr
				50					55					60
Val	Cys	Gly	Ile	Glu	Cys	Gln	Lys	Glu	Leu	Pro	Thr	Pro	Ser	Leu
				65					70					75
Ser	Glu	Leu	Glu	Asp	Tyr	Leu	Ser	Tyr	Glu	Thr	Val	Phe	Glu	Asn
				80					85					90
Gly	Thr	Arg	Thr	Leu	Thr	Arg	Val	Lys	Val	Gln	Asp	Leu	Val	Leu
				95					100					105
Glu	Pro	Thr	Gln	Asn	Ile	Thr	Thr	Lys	Gly	Val	Ser	Val	Arg	Arg
				110					115					120
Lys	Arg	Gln	Val	Tyr	Gly	Thr	Asp	Ser	Arg	Phe	Ser	Ile	Leu	Asp
				125					130					135
Lys	Arg	Phe	Leu	Thr	Asn	Phe	Pro	Phe	Ser	Thr	Ala	Val	Lys	Leu
				140					145					150
Ser	Thr	Gly	Cys	Ser	Gly	Ile	Leu	Ile	Ser	Pro	Gln	His	Val	Leu
				155					160					165
Thr	Ala	Ala	His	Cys	Val	His	Asp	Gly	Lys	Asp	Tyr	Val	Lys	Gly
				170					175					180
Ser	Lys	Lys	Leu	Arg	Val	Gly	Leu	Leu	Lys	Met	Arg	Asn	Lys	Ser
				185					190					195
Gly	Gly	Lys	Lys	Arg	Arg	Gly	Ser	Lys	Arg	Ser	Arg	Arg	Glu	Ala
				200					205					210

Ser Gly Gly Asp Gln Arg Glu Gly Thr Arg Glu His Leu Gln Glu  
 215 220 225  
 Arg Ala Lys Gly Gly Arg Arg Arg Lys Lys Ser Gly Arg Gly Gln  
 230 235 240  
 Arg Ile Ala Glu Gly Arg Pro Ser Phe Gln Trp Thr Arg Val Lys  
 245 250 255  
 Asn Thr His Ile Pro Lys Gly Trp Ala Arg Gly Gly Met Gly Asp  
 260 265 270  
 Ala Thr Leu Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Arg Ala  
 275 280 285  
 His Lys Lys Lys Tyr Met Glu Leu Gly Ile Ser Pro Thr Ile Lys  
 290 295 300  
 Lys Met Pro Gly Gly Met Ile His Phe Ser Gly Phe Asp Asn Asp  
 305 310 315  
 Arg Ala Asp Gln Leu Val Tyr Arg Phe Cys Ser Val Ser Asp Glu  
 320 325 330  
 Ser Asn Asp Leu Leu Tyr Gln Tyr Cys Asp Ala Glu Ser Gly Ser  
 335 340 345  
 Thr Gly Ser Gly Val Tyr Leu Arg Leu Lys Asp Pro Asp Lys Lys  
 350 355 360  
 Asn Trp Lys Arg Lys Ile Ile Ala Val Tyr Ser Gly His Gln Trp  
 365 370 375  
 Val Asp Val His Gly Val Gln Lys Asp Tyr Asn Val Ala Val Arg  
 380 385 390  
 Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Leu Trp Ile His Gly  
 395 400 405  
 Asn Asp Ala Asn Cys Ala Tyr Gly  
 410

<210> 297

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 297

gcattctgcag gagagagcga aggg 24

<210> 298

<211> 24

<212> DNA

<213> Artificial Sequence



<220>  
<223> Synthetic oligonucleotide probe

<400> 298  
catcggtccc gtgaatccag aggc 24

<210> 299  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 299  
gaaggagggc cttcctttca gtggacccgg gtcaagaata cccac 45

<210> 300  
<211> 1869  
<212> DNA  
<213> Homo sapiens

404301 = 130600  
<400> 300  
aatgtgagag gggctgatgg aagctgatag gcaggactgg agtgtagca 50  
ccagtactgg atgtgacagc aggcagagga gcacttagca gcttattcag 100  
tgtccgattc tgattccggc aaggatccaa gcatggaatg ctgccgtcgg 150  
gcaactcctg gcacactgct cctctttctg gctttcctgc tcttgagttc 200  
caggaccgca cgctccgagg aggaccggga cggcctatgg gatgcctggg 250  
gccccatggag tgaatgctca cgcacctgcg ggggaggggc ctactactct 300  
ctgaggcgct gcttgagcag caagagctgt gaaggaagaa atatccgata 350  
cagaacatgc agtaatgtgg actgccacc agaagcaggt gatttccgag 400  
ctcagcaatg ctcagctcat aatgatgtca agcaccatgg ccagttttat 450  
gaatggcttc ctgtgtctaa tgaccctgac aacctatgtt cactcaagtg 500  
ccaagccaaa ggaacaaccc tggttgttga actagcacct aaggcttag 550  
atgggtacgc ttgctataca gaatctttgg atatgtgcat cagtgggtta 600  
tgccaaattg ttggctgcga tcaccagctg ggaagcaccg tcaaggaaga 650  
taactgtggg gtctgcaacg gagatgggtc cacctgccgg ctggtccgag 700  
ggcagtataa atcccagctc tccgcaacca aatcgatga tactgtggtt 750  
gcatttcct atggaagtag acatattcgc cttgtcttaa aaggctcctga 800  
tcatttatat ctggaaacca aaacctcca ggggactaaa ggtgaaaaca 850  
gtctcagctc cacaggaact ttccttgtgg acaattctag tgtggacttc 900

cagaaatttc	cagacaaaga	gatactgaga	atggctggac	cactcacagc	950
agatttcatt	gtcaagattc	gtaactcggg	ctccgctgac	agtacagtcc	1000
agttcatctt	ctatcaaccc	atcatccacc	gatggaggga	gacggatttc	1050
tttccttgct	cagcaacctg	tggaggaggt	tatcagctga	catcggctga	1100
gtgctacgat	ctgaggagca	accgtgtggt	tgctgaccaa	tactgtcact	1150
attaccaga	gaacatcaaa	cccaaacc	agcttcagga	gtgcaacttg	1200
gatccttgct	cagccagtga	cggatacaag	cagatcatgc	cttatgacct	1250
ctaccatccc	cttcctcggg	gggaggccac	cccatggacc	gcgtgctcct	1300
cctcgtgtgg	ggggggcatc	cagagccggg	cagtttcctg	tgtggaggag	1350
gacatccagg	ggcatgtcac	ttcagtggaa	gagtggaaat	gcctgtacac	1400
ccctaagatg	cccacgcgc	agccctgcaa	catttttgac	tgccctaaat	1450
ggctggcaca	ggagtgggtc	ccgtgcacag	tgacatgtgg	ccagggcctc	1500
agataccgtg	tggctcctctg	catcgaccat	cgaggaatgc	acacaggagg	1550
ctgtagccca	aaaacaaagc	cccacataaa	agaggaatgc	atcgtaccca	1600
ctccctgcta	taaaccctaa	gagaaacttc	cagtcgaggc	caagttgcca	1650
tggttcaaac	aagctcaaga	gctagaagaa	ggagctgctg	tgtcagagga	1700
gccctcgtaa	gttgtaaaag	cacagactgt	tctatatttg	aaactgtttt	1750
gtttaaagaa	agcagtgtct	cactggttgt	agctttcatg	ggttctgaac	1800
taagtgtaat	catctcacca	aagctttttg	gctctcaa	taaagattga	1850
ttagtttcaa	aaaaaaaa	1869			

<210> 301

<211> 525

<212> PRT

<213> Homo sapiens

<400> 301

Met Glu Cys Cys Arg Arg Ala Thr Pro Gly Thr Leu Leu Leu Phe  
1 5 10 15

Leu Ala Phe Leu Leu Leu Ser Ser Arg Thr Ala Arg Ser Glu Glu  
20 25 30

Asp Arg Asp Gly Leu Trp Asp Ala Trp Gly Pro Trp Ser Glu Cys  
35 40 45

Ser Arg Thr Cys Gly Gly Gly Ala Ser Tyr Ser Leu Arg Arg Cys  
50 55 60

Leu Ser Ser Lys Ser Cys Glu Gly Arg Asn Ile Arg Tyr Arg Thr  
 65 70 75  
 Cys Ser Asn Val Asp Cys Pro Pro Glu Ala Gly Asp Phe Arg Ala  
 80 85 90  
 Gln Gln Cys Ser Ala His Asn Asp Val Lys His His Gly Gln Phe  
 95 100 105  
 Tyr Glu Trp Leu Pro Val Ser Asn Asp Pro Asp Asn Pro Cys Ser  
 110 115 120  
 Leu Lys Cys Gln Ala Lys Gly Thr Thr Leu Val Val Glu Leu Ala  
 125 130 135  
 Pro Lys Val Leu Asp Gly Thr Arg Cys Tyr Thr Glu Ser Leu Asp  
 140 145 150  
 Met Cys Ile Ser Gly Leu Cys Gln Ile Val Gly Cys Asp His Gln  
 155 160 165  
 Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly Val Cys Asn Gly  
 170 175 180  
 Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr Lys Ser Gln  
 185 190 195  
 Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala Leu Pro Tyr  
 200 205 210  
 Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp His Leu  
 215 220 225  
 Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser  
 230 235 240  
 Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp  
 245 250 255  
 Phe Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro  
 260 265 270  
 Leu Thr Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala  
 275 280 285  
 Asp Ser Thr Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg  
 290 295 300  
 Trp Arg Glu Thr Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly  
 305 310 315  
 Gly Tyr Gln Leu Thr Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn  
 320 325 330  
 Arg Val Val Ala Asp Gln Tyr Cys His Tyr Tyr Pro Glu Asn Ile  
 335 340 345  
 Lys Pro Lys Pro Lys Leu Gln Glu Cys Asn Leu Asp Pro Cys Pro

350	355	360
Ala Ser Asp Gly Tyr Lys Gln Ile Met	Pro Tyr Asp Leu Tyr His	
365	370	375
Pro Leu Pro Arg Trp Glu Ala Thr Pro	Trp Thr Ala Cys Ser Ser	
380	385	390
Ser Cys Gly Gly Gly Ile Gln Ser Arg	Ala Val Ser Cys Val Glu	
395	400	405
Glu Asp Ile Gln Gly His Val Thr Ser	Val Glu Glu Trp Lys Cys	
410	415	420
Met Tyr Thr Pro Lys Met Pro Ile Ala	Gln Pro Cys Asn Ile Phe	
425	430	435
Asp Cys Pro Lys Trp Leu Ala Gln Glu	Trp Ser Pro Cys Thr Val	
440	445	450
Thr Cys Gly Gln Gly Leu Arg Tyr Arg	Val Val Leu Cys Ile Asp	
455	460	465
His Arg Gly Met His Thr Gly Gly Cys	Ser Pro Lys Thr Lys Pro	
470	475	480
His Ile Lys Glu Glu Cys Ile Val Pro	Thr Pro Cys Tyr Lys Pro	
485	490	495
Lys Glu Lys Leu Pro Val Glu Ala Lys	Leu Pro Trp Phe Lys Gln	
500	505	510
Ala Gln Glu Leu Glu Glu Gly Ala Ala	Val Ser Glu Glu Pro Ser	
515	520	525

Footnote: 1302

<210> 302  
 <211> 1533  
 <212> DNA  
 <213> Homo sapiens

<400> 302  
 cggacgcgtg ggcggcggct gcggaactcc cgtggagggg ccggtgggcc 50  
 ctcgggcctg acagatggca gtggccactg cggcggcagt actggccgct 100  
 ctgggcgggg cgctgtggct ggcgcccccgc cgttcgtgg ggcccagggt 150  
 ccagcggctg cgcagaggcg gggaccccgc cctcatgcac ggaagactg 200  
 tgctgatcac cggggcgaac agcggcctgg gccgcgccac ggccgcccag 250  
 ctactgcgcc tgggagcgcg ggtgatcatg ggctgccggg accgcgcgcg 300  
 cgccgaggag gcggcgggtc agctccgcgc cgagctccgc caggccgcgcg 350  
 agtgccggcc agagcctggc gtcagcgggg tggcgagct catagtccgcg 400  
 gagctggacc tcgcctcgct gcgctcggtg cgcgccttct gccaggaaat 450

gctccaggaa gagcctaggc tggatgtctt gatcaataac gcagggatct 500  
 tccagtgtcc ttacatgaag actgaagatg ggtttgagat gcagttcgga 550  
 gtgaaccatc tggggcactt tctactcacc aatcttctcc ttggactcct 600  
 caaaagtcca gctcccagca ggattgtggt agtttcttcc aaactttata 650  
 aatacggaga catcaatttt gatgacttga acagtgaaca aagctataat 700  
 aaaagctttt gttatagccg gagcaaactg gctaacattc tttttaccag 750  
 ggaactagcc cgccgcttag aaggcacaaa tgtcacogtc aatgtgttgc 800  
 atcctggtat tgtacggaca aatctgggga ggcacataca cattccactg 850  
 ttggtcaaac cactcttcaa tttggtgtca tgggcttttt tcaaaactcc 900  
 agtagaaggt gccagactt ccatttattt ggctcttcca cctgaggtag 950  
 aaggagtgtc aggaagatac tttggggatt gtaaagagga agaactgttg 1000  
 cccaaagcta tggatgaatc tgttgcaaga aaactctggg atatcagtga 1050  
 agtgatggtt ggctgtctaa aataggaaca aggagtaaaa gagctgttta 1100  
 taaaactgca tatcagttat atctgtgatc aggaatggtg tggattgaga 1150  
 acttgttact tgaagaaaaa gaattttgat attggaatag cctgctaaga 1200  
 ggtacatgtg ggtatttttg agttactgaa aaattatttt tgggataaga 1250  
 gaatttcagc aaagatgttt taaatatata tagtaagtat aatgaataat 1300  
 aagtacaatg aaaaatacaa ttatattgta aaattataac tgggcaagca 1350  
 tggatgacat attaataatt gtcagaatta agtgactcaa agtgctatcg 1400  
 agaggttttt caagtatctt tgagtttcat ggccaaagtg ttaactagtt 1450  
 ttactacaat gtttgggtgt tgtgtggaaa ttatctgcct ggtgtgtgca 1500  
 cacaagtctt acttggaata aatttactgg tac 1533

<210> 303  
 <211> 336  
 <212> PRT  
 <213> Homo sapiens

<400> 303  
 Met Ala Val Ala Thr Ala Ala Ala Val Leu Ala Ala Leu Gly Gly  
 1 5 10 15  
 Ala Leu Trp Leu Ala Ala Arg Arg Phe Val Gly Pro Arg Val Gln  
 20 25 30  
 Arg Leu Arg Arg Gly Gly Asp Pro Gly Leu Met His Gly Lys Thr  
 35 40 45

Val Leu Ile Thr Gly Ala Asn Ser Gly Leu Gly Arg Ala Thr Ala  
50 55 60

Ala Glu Leu Leu Arg Leu Gly Ala Arg Val Ile Met Gly Cys Arg  
65 70 75

Asp Arg Ala Arg Ala Glu Glu Ala Ala Gly Gln Leu Arg Arg Glu  
80 85 90

Leu Arg Gln Ala Ala Glu Cys Gly Pro Glu Pro Gly Val Ser Gly  
95 100 105

Val Gly Glu Leu Ile Val Arg Glu Leu Asp Leu Ala Ser Leu Arg  
110 115 120

Ser Val Arg Ala Phe Cys Gln Glu Met Leu Gln Glu Glu Pro Arg  
125 130 135

Leu Asp Val Leu Ile Asn Asn Ala Gly Ile Phe Gln Cys Pro Tyr  
140 145 150

Met Lys Thr Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His  
155 160 165

Leu Gly His Phe Leu Leu Thr Asn Leu Leu Leu Gly Leu Leu Lys  
170 175 180

Ser Ser Ala Pro Ser Arg Ile Val Val Val Ser Ser Lys Leu Tyr  
185 190 195

Lys Tyr Gly Asp Ile Asn Phe Asp Asp Leu Asn Ser Glu Gln Ser  
200 205 210

Tyr Asn Lys Ser Phe Cys Tyr Ser Arg Ser Lys Leu Ala Asn Ile  
215 220 225

Leu Phe Thr Arg Glu Leu Ala Arg Arg Leu Glu Gly Thr Asn Val  
230 235 240

Thr Val Asn Val Leu His Pro Gly Ile Val Arg Thr Asn Leu Gly  
245 250 255

Arg His Ile His Ile Pro Leu Leu Val Lys Pro Leu Phe Asn Leu  
260 265 270

Val Ser Trp Ala Phe Phe Lys Thr Pro Val Glu Gly Ala Gln Thr  
275 280 285

Ser Ile Tyr Leu Ala Ser Ser Pro Glu Val Glu Gly Val Ser Gly  
290 295 300

Arg Tyr Phe Gly Asp Cys Lys Glu Glu Glu Leu Leu Pro Lys Ala  
305 310 315

Met Asp Glu Ser Val Ala Arg Lys Leu Trp Asp Ile Ser Glu Val  
320 325 330

Met Val Gly Leu Leu Lys

<210> 304  
 <211> 521  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 20, 34, 62, 87, 221, 229  
 <223> unknown base

<400> 304  
 ggggattgta aagaggaagn actgtgccca aagntatgga tgaatctgtt 50  
 gcaagaaaat tntgggatat cagtgaagtg atggttngcc tgctaaaata 100  
 ggaacaagga gtaaaagagc tgtttataaa actgcatatc agttatatct 150  
 gtgatcagga atggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200  
 tttgatattg gaatagcctg ntaagaggna catgtgggta ttttgagatt 250  
 actgaaaaat tatttttggg ataagagaat ttcagcaaag atgttttaaa 300  
 tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350  
 attgtaaaat tataactggg caagcatgga tgacatatta atatttgtca 400  
 gaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450  
 tttcatggcc aaagtgttaa ctagttttac tacaatgttt ggtgtttgtg 500  
 tggaaattat ctgcctggct t 521

<210> 305  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 305  
 ccaggaaatg ctccaggaag agcc 24

<210> 306  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 306  
 gcccatgaca ccaaattgaa gagtgg 26

<210> 307

<211> 45  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe

<400> 307  
 aacgcaggga tcttccagtg cccttacatg aagactgaag atggg 45

<210> 308  
 <211> 1523  
 <212> DNA  
 <213> Homo sapiens

<400> 308  
 gagaggacga ggtgccgtg cctggagaat cctccgtgc cgtcggctcc 50  
 cgagagccag ccctttccta acccaaccca acctagccca gtcccagccg 100  
 ccagcgctg tccctgtcac ggacccagc gttaccatgc atcctgccgt 150  
 cttcctatcc ttaccgacc tcagatgctc cttctgtgc ctggttaactt 200  
 gggtttttac tcctgtaaca actgaaataa caagtcttgc tacagagaat 250  
 atagatgaaa ttttaacaa tgctgatgtt gctttagtaa atttttatgc 300  
 tgactgggtg cgtttcagtc agatgttgca tccaattttt gaggaagctt 350  
 ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 400  
 agagttagatt gtgatcagca ctctgacata gccagagat acaggataag 450  
 caaatacca accctcaa atgtttcgtaa tgggatgatg atgaagagag 500  
 aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggcaa 550  
 caaaaaagt accccattca agaaattcgg gacttagcag aaatcaccac 600  
 tcttgatcgc agcaaaagaa atatcattgg atattttgag caaaaggact 650  
 cgacaacta tagagttttt gaacgagtag cgaatatttt gcatgatgac 700  
 tgtgcctttc tttctgcatt tggggatgtt tcaaaaccgg aaagatatag 750  
 tggcgacaac ataatctaca aaccaccagg gcattctgct ccggatatgg 800  
 tgtacttggg agctatgaca aattttgatg tgacttaca ttggattcaa 850  
 gataaatgtg ttcctcttgt ccgagaaata acatttgaaa atggagagga 900  
 attgacagaa gaaggactgc cttttctcat actctttcac atgaagaag 950  
 atacagaaag tttagaaata ttccagaatg aagtagctcg gcaattaata 1000  
 agtgaaaaag gtacaataaa ctttttacat gccgattgtg acaaatttag 1050



acatcctctt ctgcacatac agaaaactcc agcagattgt cctgtaatcg 1100  
ctattgacag ctttaggcac atgtatgtgt ttggagactt caaagatgta 1150  
ttaattcctg gaaaactcaa gcaattcgta ttgacttac attctggaaa 1200  
actgcacaga gaattccatc atggacctga cccaactgat acagccccag 1250  
gagagcaagc ccaagatgta gcaagcagtc cacctgagag ctccttcacg 1300  
aaactagcac ccagtgaata taggtatact ctattgaggg atcgagatga 1350  
gctttaaaaa cttgaaaaac agtttgtaag cctttcaaca gcagcatcaa 1400  
cctacgtggt ggaaatagta aacctatatt ttcataattc tatgtgtatt 1450  
tttattttga ataaacagaa agaaatttaa aaaaaaaaaa aaaaaaaaaa 1500  
aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309  
<211> 406  
<212> PRT  
<213> Homo sapiens

<400> 309

Met	His	Pro	Ala	Val	Phe	Leu	Ser	Leu	Pro	Asp	Leu	Arg	Cys	Ser	1	5	10	15
Leu	Leu	Leu	Leu	Val	Thr	Trp	Val	Phe	Thr	Pro	Val	Thr	Thr	Glu	20	25	30	
Ile	Thr	Ser	Leu	Ala	Thr	Glu	Asn	Ile	Asp	Glu	Ile	Leu	Asn	Asn	35	40	45	
Ala	Asp	Val	Ala	Leu	Val	Asn	Phe	Tyr	Ala	Asp	Trp	Cys	Arg	Phe	50	55	60	
Ser	Gln	Met	Leu	His	Pro	Ile	Phe	Glu	Glu	Ala	Ser	Asp	Val	Ile	65	70	75	
Lys	Glu	Glu	Phe	Pro	Asn	Glu	Asn	Gln	Val	Val	Phe	Ala	Arg	Val	80	85	90	
Asp	Cys	Asp	Gln	His	Ser	Asp	Ile	Ala	Gln	Arg	Tyr	Arg	Ile	Ser	95	100	105	
Lys	Tyr	Pro	Thr	Leu	Lys	Leu	Phe	Arg	Asn	Gly	Met	Met	Met	Lys	110	115	120	
Arg	Glu	Tyr	Arg	Gly	Gln	Arg	Ser	Val	Lys	Ala	Leu	Ala	Asp	Tyr	125	130	135	
Ile	Arg	Gln	Gln	Lys	Ser	Asp	Pro	Ile	Gln	Glu	Ile	Arg	Asp	Leu	140	145	150	
Ala	Glu	Ile	Thr	Thr	Leu	Asp	Arg	Ser	Lys	Arg	Asn	Ile	Ile	Gly	155	160	165	

Tyr Phe Glu Gln Lys Asp Ser Asp Asn Tyr Arg Val Phe Glu Arg  
170 175 180

Val Ala Asn Ile Leu His Asp Asp Cys Ala Phe Leu Ser Ala Phe  
185 190 195

Gly Asp Val Ser Lys Pro Glu Arg Tyr Ser Gly Asp Asn Ile Ile  
200 205 210

Tyr Lys Pro Pro Gly His Ser Ala Pro Asp Met Val Tyr Leu Gly  
215 220 225

Ala Met Thr Asn Phe Asp Val Thr Tyr Asn Trp Ile Gln Asp Lys  
230 235 240

Cys Val Pro Leu Val Arg Glu Ile Thr Phe Glu Asn Gly Glu Glu  
245 250 255

Leu Thr Glu Glu Gly Leu Pro Phe Leu Ile Leu Phe His Met Lys  
260 265 270

Glu Asp Thr Glu Ser Leu Glu Ile Phe Gln Asn Glu Val Ala Arg  
275 280 285

Gln Leu Ile Ser Glu Lys Gly Thr Ile Asn Phe Leu His Ala Asp  
290 295 300

Cys Asp Lys Phe Arg His Pro Leu Leu His Ile Gln Lys Thr Pro  
305 310 315

Ala Asp Cys Pro Val Ile Ala Ile Asp Ser Phe Arg His Met Tyr  
320 325 330

Val Phe Gly Asp Phe Lys Asp Val Leu Ile Pro Gly Lys Leu Lys  
335 340 345

Gln Phe Val Phe Asp Leu His Ser Gly Lys Leu His Arg Glu Phe  
350 355 360

His His Gly Pro Asp Pro Thr Asp Thr Ala Pro Gly Glu Gln Ala  
365 370 375

Gln Asp Val Ala Ser Ser Pro Pro Glu Ser Ser Phe Gln Lys Leu  
380 385 390

Ala Pro Ser Glu Tyr Arg Tyr Thr Leu Leu Arg Asp Arg Asp Glu  
395 400 405

Leu

<210> 310

<211> 182

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 36, 48  
<223> unknown base

<400> 310  
attaaggaag aatttccaaa tgaaatcaa gtagtntttg ccagagtnga 50  
ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100  
caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150  
ggtcagcgat cagtgaagc attggcagat ta 182

<210> 311  
<211> 598  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396  
<223> unknown base

TECHNOT-BIO-FOOT  
<400> 311  
agaggcctct ctggaagttg tcccgggtgt tcgccgngg agcccgggtc 50  
gagaggacna ggtgccgtg cctggagaat cctccgtgc cgtcggctcc 100  
cggagcccag ccctttccta acccaacca acctagccn gtcccagccg 150  
ccagcgctg tccctgtcnc gganccagc gtnaccatgc atcctgccgt 200  
cttctatcc ttaccgacc tcagatgctc cttctgctc ctggtactt 250  
gggtttttac tcctgtaaca actgaaataa cnngtcttga tacnnagaat 300  
atagatgaaa ttttaacna tgctgatgtg gctttagtca atttttatgc 350  
tgactggtgt cgtttcagtc agatgtggca tccaattttt gaggangctt 400  
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 450  
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 500  
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 550  
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

<210> 312  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 312  
tgagaggcct ctctggaagt tg 22

<210> 313  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 313  
gtcagcgatc agtgaaagc 19

<210> 314  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 314  
ccagaatgaa gtagctcggc 20

<210> 315  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 315  
ccgactcaaa atgcattgtc 20

<210> 316  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 316  
catttggcag gaattgtcc 19

<210> 317  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 317  
ggtgctatag gccaaagg 18

<210> 318  
<211> 24  
<212> DNA

<213> Artificial Sequence  
 <220>  
 <223> Synthetic oligonucleotide probe  
 <400> 318  
 ctgtatctct gggctatgtc agag 24  
 <210> 319  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic oligonucleotide probe  
 <400> 319  
 ctacatataa tggcacatgt cagcc 25  
 <210> 320  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic oligonucleotide probe  
 <400> 320  
 cgtcttcta tccttaccg acctcagatg ctcccttctg ctctg 46  
 <210> 321  
 <211> 1333  
 <212> DNA  
 <213> Homo sapiens  
 <400> 321  
 gcccacgcgt ccgatggcgt tcacgttcgc ggccttctgc tacatgctgg 50  
 cgctgctgct cactgccgcg ctcatcttct tcgccatttg gcacattata 100  
 gcatttgatg agctgaagac tgattacaag aatcctatag accagtgtaa 150  
 taccctgaat ccccttgtag tcccagagta cctcatccac gctttcttct 200  
 gtgtcatgtt tctttgtgca gcagagtggc ttacactggg tctcaatatg 250  
 cccctcttgg catatcatat ttggaggat atgagtagac cagtgatgag 300  
 tggcccagga ctctatgacc ctacaacat catgaatgca gatattctag 350  
 catattgtca gaaggaagga tggtgcaaat tagcttttta tcttctagca 400  
 ttttttact acctatatgg catgatctat gttttggtga gctcttagaa 450  
 caacacacag aagaattggt ccagttaagt gcatgcaaaa agccacaaa 500  
 tgaagggatt ctatccagca agatcctgtc caagagtagc ctgtggaatc 550



Ile Met Asn Ala Asp Ile Leu Ala Tyr Cys Gln Lys Glu Gly Trp  
 110 115 120  
 Cys Lys Leu Ala Phe Tyr Leu Leu Ala Phe Phe Tyr Tyr Leu Tyr  
 125 130 135  
 Gly Met Ile Tyr Val Leu Val Ser Ser  
 140

<210> 323  
 <211> 477  
 <212> DNA  
 <213> Homo sapiens

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 tgtaataccc tgaatcccct tgtactccca gagtacctca tccacgcttt 100  
 cttctgtgtc atgtttcttt gtgcagcaga gtggcttaca ctgggtctca 150  
 atatgccct cttggcatat catatttggg ggtatatgag tagaccagt 200  
 atgagtggcc caggactcta tgaccctaca accatcatga atgcagatat 250  
 tctagcatat tgcagaagg aaggatggtg caaattagct ttttatcttc 300  
 tagcattttt ttactaccta tatggcatga tctatgtttt ggtgagctct 350  
 tagaacaaca cacagaagaa ttggtccagt taagtgcag caaaaagcca 400  
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 gaatctgatc agttacttta aaaaatg 477

<210> 324  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

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<210> 325  
 <211> 41  
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 <213> Artificial Sequence

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 <223> Synthetic oligonucleotide probe

<400> 325  
 caggaaacag ctatgaccac ctgcacacct gcaaaccat t 41

<210> 326

<211> 20  
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<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 326  
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<210> 327  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 327  
actggaccaa ttcttctgtg 20

<210> 328  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 328  
gatattctag catattgtca gaaggaagga tgggtgcaaat tagct 45

<210> 329  
<211> 1174  
<212> DNA  
<213> Homo sapiens

<400> 329  
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ggacccaact ggggctcccg ccgctgctgc tgctgaccat ggccttggcc 150  
ggaggttcgg ggaccgcttc ggctgaagca tttgactcgg tcttgggtga 200  
tacggcgtct tgccaccggg cctgtcagtt gacctacccc ttgcacacct 250  
accctaagga agaggagttg tacgcatgtc agagaggttg caggctgttt 300  
tcaatttgtc agtttgtgga tgatggaatt gacttaaato gaactaaatt 350  
ggaatgtgaa tctgcatgta cagaagcata ttccaatct gatgagcaat 400  
atgcttgcca tcttggttgc cagaatcagc tgccattcgc tgaactgaga 450  
caagaacaac ttatgtocct gatgccaaaa atgcacctac tctttcctct 500



aactctggtg aggtcattct ggagtgcacat gatggactcc gcacagagct 550  
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caaataaagt tactcaaac tgtg 1174

<210> 330

<211> 323

<212> PRT

<213> Homo sapiens

<400> 330

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			20						25				30	
Gly	Thr	Ala	Ser	Ala	Glu	Ala	Phe	Asp	Ser	Val	Leu	Gly	Asp	Thr
			35						40				45	
Ala	Ser	Cys	His	Arg	Ala	Cys	Gln	Leu	Thr	Tyr	Pro	Leu	His	Thr
			50						55				60	
Tyr	Pro	Lys	Glu	Glu	Glu	Leu	Tyr	Ala	Cys	Gln	Arg	Gly	Cys	Arg
			65						70				75	
Leu	Phe	Ser	Ile	Cys	Gln	Phe	Val	Asp	Asp	Gly	Ile	Asp	Leu	Asn
			80						85				90	
Arg	Thr	Lys	Leu	Glu	Cys	Glu	Ser	Ala	Cys	Thr	Glu	Ala	Tyr	Ser
			95						100				105	
Gln	Ser	Asp	Glu	Gln	Tyr	Ala	Cys	His	Leu	Gly	Cys	Gln	Asn	Gln
			110						115				120	

protein = 4304.000

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				125					130					135	
Pro	Lys	Met	His	Leu	Leu	Phe	Pro	Leu	Thr	Leu	Val	Arg	Ser	Phe	
				140					145					150	
Trp	Ser	Asp	Met	Met	Asp	Ser	Ala	Gln	Ser	Phe	Ile	Thr	Ser	Ser	
				155					160					165	
Trp	Thr	Phe	Tyr	Leu	Gln	Ala	Asp	Asp	Gly	Lys	Ile	Val	Ile	Phe	
				170					175					180	
Gln	Ser	Lys	Pro	Glu	Ile	Gln	Tyr	Ala	Pro	His	Leu	Glu	Gln	Glu	
				185					190					195	
Pro	Thr	Asn	Leu	Arg	Glu	Ser	Ser	Leu	Ser	Lys	Met	Ser	Tyr	Leu	
				200					205					210	
Gln	Met	Arg	Asn	Ser	Gln	Ala	His	Arg	Asn	Phe	Leu	Glu	Asp	Gly	
				215					220					225	
Glu	Ser	Asp	Gly	Phe	Leu	Arg	Cys	Leu	Ser	Leu	Asn	Ser	Gly	Trp	
				230					235					240	
Ile	Leu	Thr	Thr	Thr	Leu	Val	Leu	Ser	Val	Met	Val	Leu	Leu	Trp	
				245					250					255	
Ile	Cys	Cys	Ala	Thr	Val	Ala	Thr	Ala	Val	Glu	Gln	Tyr	Val	Pro	
				260					265					270	
Ser	Glu	Lys	Leu	Ser	Ile	Tyr	Gly	Asp	Leu	Glu	Phe	Met	Asn	Glu	
				275					280					285	
Gln	Lys	Leu	Asn	Arg	Tyr	Pro	Ala	Ser	Ser	Leu	Val	Val	Val	Arg	
				290					295					300	
Ser	Lys	Thr	Glu	Asp	His	Glu	Glu	Ala	Gly	Pro	Leu	Pro	Thr	Lys	
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Val	Asn	Leu	Ala	His	Ser	Glu	Ile								
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<210> 331  
 <211> 350  
 <212> DNA  
 <213> Homo sapiens

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 ggctgttttc aatttgtcag tttgtggatg atggaattga cttaaactga 150  
 actaaattgg aatgtgaatc tgcatgtaca gaagcatatt cccaatctga 200  
 tgagcaatat gcttgccatc ttggttgcca gaatcagctg ccattcgctg 250

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<210> 332  
<211> 562  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 47  
<223> unknown base

<400> 332  
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aaacagcaac aagctgagct gctgtgacag agggacaag atggcggcgc 100  
cgaaggagc ctttgggtga ggaaccaact ggggtcccg ccgctgctgc 150  
tgctgaccat ggccttgcc ggaggttcgg ggaccgttc ggctgaagca 200  
tttgactcgg tcttgggtga tacggcgtct tgccaccggg cctgtcagtt 250  
gacctacccc ttgcacacct accctaagga agaggagttg tacgcatgtc 300  
agagaggttg caggctgttt tcaatttgc agtttgtgga tgatggaatt 350  
gacttaaadc gaactaaatt ggaatgtgaa tctgcatgta cagaagcata 400  
ttcccaatct gatgagcaat atgcttgcca tcttgggtgc cagaatcagc 450  
tgccattcgc tgaactgaga caagaacaac ttatgtccct gatgcaaaa 500  
atgcacctac tcttctct aactctggtg aggtcattct ggagtacat 550  
gatggactcc gc 562

<210> 333  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 333  
acaagctgag ctgctgtgac ag 22

<210> 334  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 334  
tgattctggc aaccaagatg gc 22

<210> 335  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 335  
atggccttgg ccggagggtc ggggaccgct tcggctgaag 40

<210> 336  
<211> 1885  
<212> DNA  
<213> Homo sapiens

<400> 336  
gcgaggtggc gatcgctgag aggcaggagg gccgaggcgg gcctgggagg 50  
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agggcgcacg gcccgcgacc gagcgtgcgg actggcctcc caagcgtggg 150  
gcgacaagct gccggagctg caatgggccc cggctgggga ttcttgttt 200  
gcctcctggg cgccgtgtgg ctgctcagct cgggccacgg agaggagcag 250  
cccccgga cagcggcaca gaggtgcttc tgccaggtta gtggttactt 300  
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tacaaggtaa acctgaagag gccgtgtcct ttctggaatg acatcagcca 450  
gtgtggaaga agggactgtg ctgtcaaacc atgtcaatct gatgaagttc 500  
ctgatggaat taaatctgcg agctacaagt attctgaaga agccaataat 550  
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accagatgct tggaaaaatat ggaatgtcat ctacgaagaa aactgtttta 800  
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acaagtgaag agaacacttt ttacagttgg ctagaaggtc tctgtgtaga 900  
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tgcatttgag tgcaagatat cttttacaag agacctgggt agaaaagaaa 1000  
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 tgaaggagaa ggtccaagaa ggcttaagaa cttgtatgtt ctctacttaa 1100  
 tagaactaag ggctttatcc aaagtgttac cattcttcga gcgccagat 1150  
 ttccaactct ttactggaaa taaaattcag gatgaggaaa acaaatgtt 1200  
 acttctggaa atacttcag aaatcaagtc atttccttg cattttgatg 1250  
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 gtctatgtat aatactactg tgagtaaaag taatacttta ataattgtgt 1800  
 acaaatttta aagttaata ttgaataaaa ggaggattat caaattaaaa 1850  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1885

<210> 337  
 <211> 468  
 <212> PRT  
 <213> Homo sapiens

<400> 337  
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 Ala Ala Gln Arg Cys Phe Cys Gln Val Ser Gly Tyr Leu Asp Asp  
 35 40 45  
 Cys Thr Cys Asp Val Glu Thr Ile Asp Arg Phe Asn Asn Tyr Arg  
 50 55 60  
 Leu Phe Pro Arg Leu Gln Lys Leu Leu Glu Ser Asp Tyr Phe Arg  
 65 70 75

Tyr Tyr Lys Val Asn Leu Lys Arg Pro Cys Pro Phe Trp Asn Asp  
80 85 90

Ile Ser Gln Cys Gly Arg Arg Asp Cys Ala Val Lys Pro Cys Gln  
95 100 105

Ser Asp Glu Val Pro Asp Gly Ile Lys Ser Ala Ser Tyr Lys Tyr  
110 115 120

Ser Glu Glu Ala Asn Asn Leu Ile Glu Glu Cys Glu Gln Ala Glu  
125 130 135

Arg Leu Gly Ala Val Asp Glu Ser Leu Ser Glu Glu Thr Gln Lys  
140 145 150

Ala Val Leu Gln Trp Thr Lys His Asp Asp Ser Ser Asp Asn Phe  
155 160 165

Cys Glu Ala Asp Asp Ile Gln Ser Pro Glu Ala Glu Tyr Val Asp  
170 175 180

Leu Leu Leu Asn Pro Glu Arg Tyr Thr Gly Tyr Lys Gly Pro Asp  
185 190 195

Ala Trp Lys Ile Trp Asn Val Ile Tyr Glu Glu Asn Cys Phe Lys  
200 205 210

Pro Gln Thr Ile Lys Arg Pro Leu Asn Pro Leu Ala Ser Gly Gln  
215 220 225

Gly Thr Ser Glu Glu Asn Thr Phe Tyr Ser Trp Leu Glu Gly Leu  
230 235 240

Cys Val Glu Lys Arg Ala Phe Tyr Arg Leu Ile Ser Gly Leu His  
245 250 255

Ala Ser Ile Asn Val His Leu Ser Ala Arg Tyr Leu Leu Gln Glu  
260 265 270

Thr Trp Leu Glu Lys Lys Trp Gly His Asn Ile Thr Glu Phe Gln  
275 280 285

Gln Arg Phe Asp Gly Ile Leu Thr Glu Gly Glu Gly Pro Arg Arg  
290 295 300

Leu Lys Asn Leu Tyr Phe Leu Tyr Leu Ile Glu Leu Arg Ala Leu  
305 310 315

Ser Lys Val Leu Pro Phe Phe Glu Arg Pro Asp Phe Gln Leu Phe  
320 325 330

Thr Gly Asn Lys Ile Gln Asp Glu Glu Asn Lys Met Leu Leu Leu  
335 340 345

Glu Ile Leu His Glu Ile Lys Ser Phe Pro Leu His Phe Asp Glu  
350 355 360

Asn Ser Phe Phe Ala Gly Asp Lys Lys Glu Ala His Lys Leu Lys

	365		370		375
Glu Asp Phe Arg	Leu His Phe Arg Asn	Ile Ser Arg Ile Met Asp			
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Cys Val Gly Cys	Phe Lys Cys Arg Leu	Trp Gly Lys Leu Gln Thr			
	395	400			405
Gln Gly Leu Gly	Thr Ala Leu Lys Ile	Leu Phe Ser Glu Lys Leu			
	410	415			420
Ile Ala Asn Met	Pro Glu Ser Gly Pro	Ser Tyr Glu Phe His Leu			
	425	430			435
Thr Arg Gln Glu	Ile Val Ser Leu Phe	Asn Ala Phe Gly Arg Ile			
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Ser Thr Ser Val	Lys Glu Leu Glu Asn	Phe Arg Asn Leu Leu Gln			
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Asn Ile His					

<210> 338  
<211> 507  
<212> DNA  
<213> Homo sapiens

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<220>  
<221> unsure  
<222> 101, 263, 376, 397, 426  
<223> unknown base
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nacacttttt acagttggct agaaggtctc tgtgtagaaa aaagagcatt 150  
ctacagactt atatctggcc tacatgcaag cattaatgtg catttgagtg 200  
caagatatct tttaacaagag acctggttag aaaagaaatg gggacacaac 250  
attacagaat ttnaacagcg atttgatgga attttgactg aaggagaagg 300  
tccaagaagg cttaagaact tgtattttct ctacttaata gaactaaggg 350  
ctttatccaa agtgttacca ttcttngagc gccagagatt tcaactnttt 400  
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tttgctg 507

<210> 339  
<211> 20

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 339  
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 <210> 340  
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 <212> DNA  
 <213> Artificial Sequence  
  
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 <223> Synthetic oligonucleotide probe  
  
 <400> 340  
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 <210> 341  
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 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 341  
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 <210> 342  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 342  
 agagattcat ccaactgctcc aagtcg 26  
  
 <210> 343  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 343  
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 <210> 344  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence



<220>  
<223> Synthetic oligonucleotide probe

<400> 344  
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<210> 345

<211> 1486

<212> DNA

<213> Homo sapiens

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ggactttctca tactggacag aaaccgatca ggcattggaac tccccttcgt 150  
cactcacctg ttcttgcccc tgggtttcct gacaggtctc tgctccccct 200  
ttaacctgga tgaacatcac ccacgcctat tcccagggcc accagaagct 250  
gaatttgat acagtgtctt acaacatgtt gggggtggac agcgatgat 300  
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cacttaggtg actaccaact gggaaattca tctcatctg ctgtgaatat 450  
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 aaaataataa taataataat tcagactcct tatcaggagt ccatgatctg 1350  
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 agaaagaccc catctctaaa taaatgtttt aaaaat 1486

<210> 346  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

<400> 346  
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 Arg Leu Phe Pro Gly Pro Pro Glu Ala Glu Phe Gly Tyr Ser Val  
 35 40 45  
 Leu Gln His Val Gly Gly Gly Gln Arg Trp Met Leu Val Gly Ala  
 50 55 60  
 Pro Trp Asp Gly Pro Ser Gly Asp Arg Arg Gly Asp Val Tyr Arg  
 65 70 75  
 Cys Pro Val Gly Gly Ala His Asn Ala Pro Cys Ala Lys Gly His  
 80 85 90  
 Leu Gly Asp Tyr Gln Leu Gly Asn Ser Ser His Pro Ala Val Asn  
 95 100 105  
 Met His Leu Gly Met Ser Leu Leu Glu Thr Asp Gly Asp Gly Gly  
 110 115 120  
 Phe Met Val Ser

<210> 347  
 <211> 509  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 22  
 <223> unknown base

<400> 347

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 ggagagggac agaggccaga ggactttctca tactggacag aaaccgatca 150  
 ggcattggaac tccccttcgt cactcacctg ttcttgcccc tgggtgttct 200  
 gacaggtctc tgctccccct ttaacctgga tgaacatcac ccacgcctat 250  
 tcccagggcc accagaagct gaatttggat acagtgtctt acaacatggt 300  
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 aggcgaccgg aggggggacg tttatcgctg ccctgtaggg ggggcccaca 400  
 atgccccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450  
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 tggtgatgg 509

<210> 348  
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 <212> DNA  
 <213> Artificial Sequence  
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 <223> Synthetic oligonucleotide probe  
 <400> 348  
 agggacagag gccagaggac ttc 23

<210> 349  
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 <212> DNA  
 <213> Artificial Sequence  
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 <223> Synthetic oligonucleotide probe  
 <400> 349  
 caggtgcata ttcacagcag gatg 24

<210> 350  
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 <220>  
 <223> Synthetic oligonucleotide probe  
 <400> 350  
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<210> 351  
 <211> 2056  
 <212> DNA

<213> Homo sapiens

<400> 351

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gcttctctggg cgggctctag aacaattcag gcttcgctgc gactcagacc 150  
tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200  
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tcttgatgtg gagcccagtg atcgcgcctg gagaaacagt gtactattct 450  
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 acggaggatc catgaactac tgtaaagtgt tgacagtgtg tgcacactgc-1900  
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 gtaacatgtg catgtttgtt gtgctccttt tttctgttgg taaagtacag 2000  
 aattcagcaa ataaaaaggg ccaccctggc caaaagcggg aaaaaaaaaa 2050  
 aaaaaa 2056

<210> 352  
 <211> 311  
 <212> PRT  
 <213> Homo sapiens

<400> 352  
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 Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp  
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 Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser  
 35 40 45  
 Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro  
 50 55 60  
 Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu  
 65 70 75  
 Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser  
 80 85 90  
 Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala  
 95 100 105  
 Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln  
 110 115 120

Thr Ser Ala Trp Ser Ile Leu Lys His Pro Phe Asn Arg Asn Ser  
 125 130 135  
 Thr Ile Leu Thr Arg Pro Gly Met Glu Ile Thr Lys Asp Gly Phe  
 140 145 150  
 His Leu Val Ile Glu Leu Glu Asp Leu Gly Pro Gln Phe Glu Phe  
 155 160 165  
 Leu Val Ala Tyr Trp Arg Arg Glu Pro Gly Ala Glu Glu His Val  
 170 175 180  
 Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu Glu Thr Met  
 185 190 195  
 Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe Val Lys  
 200 205 210  
 Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val Glu  
 215 220 225  
 Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe  
 230 235 240  
 Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp  
 245 250 255  
 Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val  
 260 265 270  
 Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile  
 275 280 285  
 Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met  
 290 295 300  
 Ser Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser  
 305 310

<210> 353  
 <211> 864  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 654, 711, 748, 827  
 <223> unknown base

<400> 353  
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 cctttctagc ttcttgccg gctctagaac aattcaggct tcgctgcgac 100  
 tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150  
 agaatgcttt attttgaaa gaaacaatgt tctaggtcaa actgagtcta 200



<400> 356  
tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 357

<211> 1670

<212> DNA

<213> Homo sapiens

<400> 357

cccacgcgtc cgcccacgcg tccgaggagc aagagagaag agagactgaa 50

acagggagaa gaggcaggag aggaggaggt ggggagagca cgaagctgga 100

ggccgacact gagggagggc gggaggaggt gaagaaggag agaggggaga 150

agaggcagga gctggaaagg agagaggag gaggaggagg agatgcggga 200

tggagacctg gagttaggtg gcttgggaga gcttaatgaa aagagaacgg 250

agaggaggtg tgggttagga accaagaggt agccctgtgg gcagcagaag 300

gctgagagga gttagaagat caggagctag agggagactg gagggttccg 350

ggaaaagagc agaggaaaga ggaaagacac agagagacgg gagagagaag 400

aagagtgggt ttgaagggcg gatctcagtc cctggctgct ttggcatttg 450

gggaactggg actccctgtg gggaggagag gaaagctgga agtcctggag 500

ggacagggtc ccagaaggag gggacagagg agctgagaga ggggggcagg 550

gcgttgggca ggggtccctc ggaggcctcc tggggatggg ggctgcagct 600

cgtctgagcg cccctcgagc gctggtactc tgggctgcac tgggggcagc 650

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ataatctoca gggaaacttc gtgccagggc ctccctttctg gggcctgggtg 750

aatgcagcgt ggagtctgtg tgctgtgggg aagcggcaga gcccctgga 800

tgtggagctg aagaggggtc tttatgaccc ctttctgccc ccattaaggc 850

tcagcactgg aggagagaag ctccggggaa ccttgtacaa caccggccga 900

catgtctcct tcctgcctgc accccgacct gtggtcaatg tgtctggagg 950

tcccctcctt tacagccacc gactcagtga actgcggctg ctgtttggag 1000

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acgttgccag tacctctaac ccattcctca gtgcctcct taaccgcgac 1200

accatcactc gcattctcta caagaatgat gcctactttc ttcaagacct 1250

FOOT = 130200T



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gaccgggccc tcaatcac ctcccttcag atgactccc tgagactcct 1400  
gagccagaat cctccatctc agatcttcca gagcctcagc ggtaacagcc 1450  
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ttaaggagac agaatactta 1670

<210> 358  
<211> 328  
<212> PRT  
<213> Homo sapiens

<400> 358  
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Pro Glu Asp Trp Trp Ser Tyr Lys Asp Asn Leu Gln Gly Asn Phe  
35 40 45  
Val Pro Gly Pro Pro Phe Trp Gly Leu Val Asn Ala Ala Trp Ser  
50 55 60  
Leu Cys Ala Val Gly Lys Arg Gln Ser Pro Val Asp Val Glu Leu  
65 70 75  
Lys Arg Val Leu Tyr Asp Pro Phe Leu Pro Pro Leu Arg Leu Ser  
80 85 90  
Thr Gly Gly Glu Lys Leu Arg Gly Thr Leu Tyr Asn Thr Gly Arg  
95 100 105  
His Val Ser Phe Leu Pro Ala Pro Arg Pro Val Val Asn Val Ser  
110 115 120  
Gly Gly Pro Leu Leu Tyr Ser His Arg Leu Ser Glu Leu Arg Leu  
125 130 135  
Leu Phe Gly Ala Arg Asp Gly Ala Gly Ser Glu His Gln Ile Asn  
140 145 150  
His Gln Gly Phe Ser Ala Glu Val Gln Leu Ile His Phe Asn Gln  
155 160 165  
Glu Leu Tyr Gly Asn Phe Ser Ala Ala Ser Arg Gly Pro Asn Gly

170	175	180
Leu Ala Ile Leu Ser Leu Phe Val Asn Val Ala Ser Thr Ser Asn		
185	190	195
Pro Phe Leu Ser Arg Leu Leu Asn Arg Asp Thr Ile Thr Arg Ile		
200	205	210
Ser Tyr Lys Asn Asp Ala Tyr Phe Leu Gln Asp Leu Ser Leu Glu		
215	220	225
Leu Leu Phe Pro Glu Ser Phe Gly Phe Ile Thr Tyr Gln Gly Ser		
230	235	240
Leu Ser Thr Pro Pro Cys Ser Glu Thr Val Thr Trp Ile Leu Ile		
245	250	255
Asp Arg Ala Leu Asn Ile Thr Ser Leu Gln Met His Ser Leu Arg		
260	265	270
Leu Leu Ser Gln Asn Pro Pro Ser Gln Ile Phe Gln Ser Leu Ser		
275	280	285
Gly Asn Ser Arg Pro Leu Gln Pro Leu Ala His Arg Ala Leu Arg		
290	295	300
Gly Asn Arg Asp Pro Arg His Pro Glu Arg Arg Cys Arg Gly Pro		
305	310	315
Asn Tyr Arg Leu His Val Asp Gly Val Pro His Gly Arg		
320	325	

Protein: h302001

<210> 359

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 359

tctgctgagg tgcagctcat tcac 24

<210> 360

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 360

gaggctctgg aagatctgag atgg 24

<210> 361

<211> 50

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 361  
gcctctttgt caacgttgcc agtacctcta acccattcct cagtcgcctc 50

<210> 362  
<211> 3038

<212> DNA

<213> Homo sapiens

<400> 362  
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gcagctactg ctacaaaacg ctggggcgcc caccctggca gactaacgaa 150  
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gagtgggtgga tagccaaaca acgagggaaa agggccatca cagacaatga 650  
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 aatgtatttg tgctttgata ctaaaaatct gtaaaatggt agttttggta 2950  
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 taaacattaa aattaatcat gtttcaaaaa aaaaaaaa 3038

<210> 363  
 <211> 500  
 <212> PRT  
 <213> Homo sapiens

<400> 363  
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 1 5 10  
 Phe Met Ala Arg Ala Ile Pro Ala Met Val Val Pro Asn Ala Thr 30  
 20 25  
 Leu Leu Glu Lys Leu Leu Glu Lys Tyr Met Asp Glu Asp Gly Glu 45  
 35 40  
 Trp Trp Ile Ala Lys Gln Arg Gly Lys Arg Ala Ile Thr Asp Asn 60  
 50 55  
 Asp Met Gln Ser Ile Leu Asp Leu His Asn Lys Leu Arg Ser Gln 75  
 65 70  
 Val Tyr Pro Thr Ala Ser Asn Met Glu Tyr Met Thr Trp Asp Val 90  
 80 85  
 Glu Leu Glu Arg Ser Ala Glu Ser Trp Ala Glu Ser Cys Leu Trp 105  
 95 100  
 Glu His Gly Pro Ala Ser Leu Leu Pro Ser Ile Gly Gln Asn Leu 120  
 110 115  
 Gly Ala His Trp Gly Arg Tyr Arg Pro Pro Thr Phe His Val Gln 135  
 125 130  
 Ser Trp Tyr Asp Glu Val Lys Asp Phe Ser Tyr Pro Tyr Glu His 150  
 140 145  
 Glu Cys Asn Pro Tyr Cys Pro Phe Arg Cys Ser Gly Pro Val Cys 165  
 155 160  
 Thr His Tyr Thr Gln Val Val Trp Ala Thr Ser Asn Arg Ile Gly

170	175	180
Cys Ala Ile Asn Leu Cys His Asn Met	Asn Ile Trp Gly Gln Ile	
185	190	195
Trp Pro Lys Ala Val Tyr Leu Val Cys	Asn Tyr Ser Pro Lys Gly	
200	205	210
Asn Trp Trp Gly His Ala Pro Tyr Lys	His Gly Arg Pro Cys Ser	
215	220	225
Ala Cys Pro Pro Ser Phe Gly Gly Gly	Cys Arg Glu Asn Leu Cys	
230	235	240
Tyr Lys Glu Gly Ser Asp Arg Tyr Tyr	Pro Pro Arg Glu Glu Glu	
245	250	255
Thr Asn Glu Ile Glu Arg Gln Gln Ser	Gln Val His Asp Thr His	
260	265	270
Val Arg Thr Arg Ser Asp Asp Ser Ser	Arg Asn Glu Val Ile Ser	
275	280	285
Ala Gln Gln Met Ser Gln Ile Val Ser	Cys Glu Val Arg Leu Arg	
290	295	300
Asp Gln Cys Lys Gly Thr Thr Cys Asn	Arg Tyr Glu Cys Pro Ala	
305	310	315
Gly Cys Leu Asp Ser Lys Ala Lys Val	Ile Gly Ser Val His Tyr	
320	325	330
Glu Met Gln Ser Ser Ile Cys Arg Ala	Ala Ile His Tyr Gly Ile	
335	340	345
Ile Asp Asn Asp Gly Gly Trp Val Asp	Ile Thr Arg Gln Gly Arg	
350	355	360
Lys His Tyr Phe Ile Lys Ser Asn Arg	Asn Gly Ile Gln Thr Ile	
365	370	375
Gly Lys Tyr Gln Ser Ala Asn Ser Phe	Thr Val Ser Lys Val Thr	
380	385	390
Val Gln Ala Val Thr Cys Glu Thr Thr	Val Glu Gln Leu Cys Pro	
395	400	405
Phe His Lys Pro Ala Ser His Cys Pro	Arg Val Tyr Cys Pro Arg	
410	415	420
Asn Cys Met Gln Ala Asn Pro His Tyr	Ala Arg Val Ile Gly Thr	
425	430	435
Arg Val Tyr Ser Asp Leu Ser Ser Ile	Cys Arg Ala Ala Val His	
440	445	450
Ala Gly Val Val Arg Asn His Gly Gly	Tyr Val Asp Val Met Pro	
455	460	465

Val Asp Lys Arg Lys Thr Tyr Ile Ala Ser Phe Gln Asn Gly Ile  
470 475 480

Phe Ser Glu Ser Leu Gln Asn Pro Pro Gly Gly Lys Ala Phe Arg  
485 490 495

Val Phe Ala Val Val  
500

<210> 364  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 364  
ggacagaatt tgggagcaca ctgg 24

<210> 365  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 365  
ccaagagtat actgtcctcg 20

<210> 366  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 366  
agcacagatt ttctctacag cccc 25

<210> 367  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 367  
aaccactcca gcatgtactg ctgc 24

<210> 368  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 368

ccattcaggt gttctggccc tgtatgtaca cattatacac aggtcgtgtg 50

<210> 369

<211> 1685

<212> DNA

<213> Homo sapiens

<400> 369

gcggagacaa gcgcagagcg cagcgcacgg ccacagacag ccctgggcat 50

ccaccgacgg cgcagccgga gccagcagag ccggaaggcg cgccccgggc 100

agagaaagcc gagcagagct ggggtggcgtc tccgggcccgc cgctccgacg 150

ggccagcggc ctcccatgt ccctgtctcc acgcccggcc cctecgggtca 200

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accgcgcgtg tggacgggtc caaatgcaag tgctcccga agggacccaa 300

gatccgctac agcgacgtga agaagctgga aatgaagcca aagtaccgcg 350

actgcgagga gaagatggtt atcatcacca ccaagagcgt gtccaggtag 400

cgaggtcagg agcactgcct gcaccccaag ctgcagagca ccaagcgctt 450

catcaagtgg tacaacgcct ggaacgagaa gcgcagggtc tacgaagaat 500

agggtgaaaa acctcagaag ggaaaaactcc aaaccagttg ggagacttgt 550

gcaaaggact ttgcagatta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 600

aaaaaaaaaa aaagcctttc tttctcacag gcataagaca caaattatat 650

attgttatga agcacttttt accaacggtc agtttttaca ttttatagct 700

gcgtgcgaaa ggcttccaga tgggagaccc atctctcttg tgctccagac 750

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<210> 370

<211> 111

<212> PRT

<213> Homo sapiens

<400> 370

Met Ser Leu Leu Pro Arg Arg Ala Pro Pro Val Ser Met Arg Leu  
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 20 25 30

Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys  
 35 40 45

Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr  
 50 55 60

Pro His Cys Glu Glu Lys Met Val Ile Ile Thr Thr Lys Ser Val  
 65 70 75

Ser Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln  
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Arg Arg Val Tyr Glu Glu  
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<210> 371

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 371

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<223> Synthetic oligonucleotide probe

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<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 373

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<210> 374

<211> 3113

<212> DNA

<213> Homo sapiens

<400> 374

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cggtttcagc cccagaacc cccgtcctcc tggactggca tccgaaatac 300

tactcagttt gctgctgtgt gccccagca cctggatgag agatccttac 350

tgcatgacat gctgcccac ttgtttaccg ccaatttga tactttgatg 400

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<211> 816

<212> PRT

<213> Homo sapiens

<400> 375

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Thr Asn Tyr Gly Lys Ile Arg Gly Leu Arg Thr Pro Leu Pro Asn  
35 40 45

Glu Ile Leu Gly Pro Val Glu Gln Tyr Leu Gly Val Pro Tyr Ala.

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Ser	Pro	Pro	Thr	Gly	Glu	Arg	Arg	Phe	Gln	Pro	Pro	Glu	Pro	Pro					
				65					70					75					
Ser	Ser	Trp	Thr	Gly	Ile	Arg	Asn	Thr	Thr	Gln	Phe	Ala	Ala	Val					
				80					85					90					
Cys	Pro	Gln	His	Leu	Asp	Glu	Arg	Ser	Leu	Leu	His	Asp	Met	Leu					
				95					100					105					
Pro	Ile	Trp	Phe	Thr	Ala	Asn	Leu	Asp	Thr	Leu	Met	Thr	Tyr	Val					
				110					115					120					
Gln	Asp	Gln	Asn	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Ile	Tyr	Val	Pro					
				125					130					135					
Thr	Glu	Asp	Gly	Ala	Asn	Thr	Lys	Lys	Asn	Ala	Asp	Asp	Ile	Thr					
				140					145					150					
Ser	Asn	Asp	Arg	Gly	Glu	Asp	Glu	Asp	Ile	His	Asp	Gln	Asn	Ser					
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Lys	Lys	Pro	Val	Met	Val	Tyr	Ile	His	Gly	Gly	Ser	Tyr	Met	Glu					
				170					175					180					
Gly	Thr	Gly	Asn	Met	Ile	Asp	Gly	Ser	Ile	Leu	Ala	Ser	Tyr	Gly					
				185					190					195					
Asn	Val	Ile	Val	Ile	Thr	Ile	Asn	Tyr	Arg	Leu	Gly	Ile	Leu	Gly					
				200					205					210					
Phe	Leu	Ser	Thr	Gly	Asp	Gln	Ala	Ala	Lys	Gly	Asn	Tyr	Gly	Leu					
				215					220					225					
Leu	Asp	Gln	Ile	Gln	Ala	Leu	Arg	Trp	Ile	Glu	Glu	Asn	Val	Gly					
				230					235					240					
Ala	Phe	Gly	Gly	Asp	Pro	Lys	Arg	Val	Thr	Ile	Phe	Gly	Ser	Gly					
				245					250					255					
Ala	Gly	Ala	Ser	Cys	Val	Ser	Leu	Leu	Thr	Leu	Ser	His	Tyr	Ser					
				260					265					270					
Glu	Gly	Leu	Phe	Gln	Lys	Ala	Ile	Ile	Gln	Ser	Gly	Thr	Ala	Leu					
				275					280					285					
Ser	Ser	Trp	Ala	Val	Asn	Tyr	Gln	Pro	Ala	Lys	Tyr	Thr	Arg	Ile					
				290					295					300					
Leu	Ala	Asp	Lys	Val	Gly	Cys	Asn	Met	Leu	Asp	Thr	Thr	Asp	Met					
				305					310					315					
Val	Glu	Cys	Leu	Arg	Asn	Lys	Asn	Tyr	Lys	Glu	Leu	Ile	Gln	Gln					
				320					325					330					
Thr	Ile	Thr	Pro	Ala	Thr	Tyr	His	Ile	Ala	Phe	Gly	Pro	Val	Ile					
				335					340					345					



635	640	645
Asn Pro Lys His Ser Lys Asp Pro His	Lys Thr Gly Pro Glu Asp	
650	655	660
Thr Thr Val Leu Ile Glu Thr Lys Arg	Asp Tyr Ser Thr Glu Leu	
665	670	675
Ser Val Thr Ile Ala Val Gly Ala Ser	Leu Leu Phe Leu Asn Ile	
680	685	690
Leu Ala Phe Ala Ala Leu Tyr Tyr Lys	Lys Asp Lys Arg Arg His	
695	700	705
Glu Thr His Arg Arg Pro Ser Pro Gln	Arg Asn Thr Thr Asn Asp	
710	715	720
Ile Ala His Ile Gln Asn Glu Glu Ile	Met Ser Leu Gln Met Lys	
725	730	735
Gln Leu Glu His Asp His Glu Cys Glu	Ser Leu Gln Ala His Asp	
740	745	750
Thr Leu Arg Leu Thr Cys Pro Pro Asp	Tyr Thr Leu Thr Leu Arg	
755	760	765
Arg Ser Pro Asp Asp Ile Pro Leu Met	Thr Pro Asn Thr Ile Thr	
770	775	780
Met Ile Pro Asn Thr Leu Thr Gly Met	Gln Pro Leu His Thr Phe	
785	790	795
Asn Thr Phe Ser Gly Gly Gln Asn Ser	Thr Asn Leu Pro His Gly	
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His Ser Thr Thr Arg Val		
815		

130201-130201

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 <213> Artificial Sequence  
  
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 <400> 376  
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 <210> 377  
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 <213> Artificial Sequence  
  
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aacccccgag ccaaaagatg gtcac 25

<210> 378

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 378

gtaccggtga ccaggcagca aaaggcaact atgggctcct ggatcag 47

<210> 379

<211> 2461

<212> DNA

<213> Homo sapiens

<400> 379

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cgagtacttg aaacgggagc actcgtctgc gaagccctac caggggtgtgg 200

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accagtata tccgccttac ccagatatg caaagtaaac aggggtgcctt 300

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gctgcctgag atgacagctc cactgccgcc cctgagtggc ctggccctct 950

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<212> PRT

<213> Homo sapiens

<400> 380

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Arg	Cys	Leu	Ser	Ala	Arg	Asp	Gly	Ser	Arg	Met	Leu	Leu	Leu	Leu
				20					25					30
Leu	Leu	Leu	Gly	Ser	Gly	Gln	Gly	Pro	Gln	Gln	Val	Gly	Ala	Gly
				35					40					45
Gln	Thr	Phe	Glu	Tyr	Leu	Lys	Arg	Glu	His	Ser	Leu	Ser	Lys	Pro
				50					55					60
Tyr	Gln	Gly	Val	Gly	Thr	Gly	Ser	Ser	Ser	Leu	Trp	Asn	Leu	Met
				65					70					75
Gly	Asn	Ala	Met	Val	Met	Thr	Gln	Tyr	Ile	Arg	Leu	Thr	Pro	Asp
				80					85					90
Met	Gln	Ser	Lys	Gln	Gly	Ala	Leu	Trp	Asn	Arg	Val	Pro	Cys	Phe
				95					100					105
Leu	Arg	Asp	Trp	Glu	Leu	Gln	Val	His	Phe	Lys	Ile	His	Gly	Gln
				110					115					120
Gly	Lys	Lys	Asn	Leu	His	Gly	Asp	Gly	Leu	Ala	Ile	Trp	Tyr	Thr
				125					130					135
Lys	Asp	Arg	Met	Gln	Pro	Gly	Pro	Val	Phe	Gly	Asn	Met	Asp	Lys
				140					145					150
Phe	Val	Gly	Leu	Gly	Val	Phe	Val	Asp	Thr	Tyr	Pro	Asn	Glu	Glu
				155					160					165
Lys	Gln	Gln	Glu	Arg	Val	Phe	Pro	Tyr	Ile	Ser	Ala	Met	Val	Asn
				170					175					180
Asn	Gly	Ser	Leu	Ser	Tyr	Asp	His	Glu	Arg	Asp	Gly	Arg	Pro	Thr
				185					190					195
Glu	Leu	Gly	Gly	Cys	Thr	Ala	Ile	Val	Arg	Asn	Leu	His	Tyr	Asp
				200					205					210
Thr	Phe	Leu	Val	Ile	Arg	Tyr	Val	Lys	Arg	His	Leu	Thr	Ile	Met
				215					220					225
Met	Asp	Ile	Asp	Gly	Lys	His	Glu	Trp	Arg	Asp	Cys	Ile	Glu	Val
				230					235					240
Pro	Gly	Val	Arg	Leu	Pro	Arg	Gly	Tyr	Tyr	Phe	Gly	Thr	Ser	Ser
				245					250					255

Ile Thr Gly Asp Leu Ser Asp Asn His Asp Val Ile Ser Leu Lys  
260 265 270

Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu Glu Glu Lys Leu  
275 280 285

His Arg Asp Val Phe Leu Pro Ser Val Asp Asn Met Lys Leu Pro  
290 295 300

Glu Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu Phe  
305 310 315

Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val  
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Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys  
335 340 345

Arg Phe Tyr

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<210> 382  
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<212> DNA  
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<400> 382  
cactctccag gctgcatgct cagg 24

<210> 383  
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<212> DNA  
<213> Artificial Sequence

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<400> 383  
gtcaaactgt cgagtacttg aaacgggagc actcgctgtc gaagc 45

<210> 384  
<211> 3150  
<212> DNA  
<213> Homo sapiens

<400> 384

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<210> 385

<211> 480

<212> PRT

<213> Homo sapiens

<400> 385

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Leu Leu Ala Phe Val Ser Leu Ser Leu Gln Phe Phe His Leu Ile  
 20 25 30

Pro Val Ser Thr Pro Lys Asn Gly Met Ser Ser Lys Ser Arg Lys  
 35 40 45

Arg Ile Met Pro Asp Pro Val Thr Glu Pro Pro Val Thr Asp Pro  
 50 55 60

Val Tyr Glu Ala Leu Leu Tyr Cys Asn Ile Pro Ser Val Ala Glu  
 65 70 75

Arg Ser Met Glu Gly His Ala Pro His His Phe Lys Leu Val Ser  
 80 85 90

Val His Val Phe Ile Arg His Gly Asp Arg Tyr Pro Leu Tyr Val  
 95 100 105

Ile Pro Lys Thr Lys Arg Pro Glu Ile Asp Cys Thr Leu Val Ala  
 110 115 120

Asn Arg Lys Pro Tyr His Pro Lys Leu Glu Ala Phe Ile Ser His  
 125 130 135

Met Ser Lys Gly Ser Gly Ala Ser Phe Glu Ser Pro Leu Asn Ser  
 140 145 150

Leu Pro Leu Tyr Pro Asn His Pro Leu Cys Glu Met Gly Glu Leu  
 155 160 165

Thr Gln Thr Gly Val Val Gln His Leu Gln Asn Gly Gln Leu Leu  
 170 175 180

Arg Asp Ile Tyr Leu Lys Lys His Lys Leu Leu Pro Asn Asp Trp  
 185 190 195

Ser Ala Asp Gln Leu Tyr Leu Glu Thr Thr Gly Lys Ser Arg Thr  
 200 205 210

TTTCTCTTGT

Leu Gln Ser Gly	Leu Ala Leu Leu Tyr	Gly Phe Leu Pro Asp	Phe
215		220	225
Asp Trp Lys Lys	Ile Tyr Phe Arg His	Gln Pro Ser Ala Leu	Phe
230		235	240
Cys Ser Gly Ser	Cys Tyr Cys Pro Val	Arg Asn Gln Tyr Leu	Glu
245		250	255
Lys Glu Gln Arg	Arg Gln Tyr Leu Leu	Arg Leu Lys Asn Ser	Gln
260		265	270
Leu Glu Lys Thr	Tyr Gly Glu Met Ala	Lys Ile Val Asp Val	Pro
275		280	285
Thr Lys Gln Leu	Arg Ala Ala Asn Pro	Ile Asp Ser Met Leu	Cys
290		295	300
His Phe Cys His	Asn Val Ser Phe Pro	Cys Thr Arg Asn Gly	Cys
305		310	315
Val Asp Met Glu	His Phe Lys Val Ile	Lys Thr His Gln Ile	Glu
320		325	330
Asp Glu Arg Glu	Arg Arg Glu Lys Lys	Leu Tyr Phe Gly Tyr	Ser
335		340	345
Leu Leu Gly Ala	His Pro Ile Leu Asn	Gln Thr Ile Gly Arg	Met
350		355	360
Gln Arg Ala Thr	Glu Gly Arg Lys Glu	Glu Leu Phe Ala Leu	Tyr
365		370	375
Ser Ala His Asp	Val Thr Leu Ser Pro	Val Leu Ser Ala Leu	Gly
380		385	390
Leu Ser Glu Ala	Arg Phe Pro Arg Phe	Ala Ala Arg Leu Ile	Phe
395		400	405
Glu Leu Trp Gln	Asp Arg Glu Lys Pro	Ser Glu His Ser Val	Arg
410		415	420
Ile Leu Tyr Asn	Gly Val Asp Val Thr	Phe His Thr Ser Phe	Cys
425		430	435
Gln Asp His His	Lys Arg Ser Pro Lys	Pro Met Cys Pro Leu	Glu
440		445	450
Asn Leu Val Arg	Phe Val Lys Arg Asp	Met Phe Val Ala Leu	Gly
455		460	465
Gly Ser Gly Thr	Asn Tyr Tyr Asp Ala	Cys His Arg Glu Gly	Phe
470		475	480

<210> 386  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 386  
ccaagcagct tagagctcca gacc 24

<210> 387  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 387  
ttccctatgc tctgtattgg catgg 25

<210> 388  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 388  
gccacttctg ccacaatgtc agctttccct gtaccagaaa tggctgtgtt 50

<210> 389  
<211> 3313  
<212> DNA  
<213> Homo sapiens

<400> 389  
aaaaaagctc actaaagttt ctattagagc gaatacggta gatttccatc 50  
cccttttgaa gaacagtact gtggagctat ttaagagata aaaacgaaat 100  
atcctttctg ggagttcaag attgtgcagt aattgggttag gactctgagc 150  
gccgctgttc accaatcggg gagagaaaag cggagatcct gctcgccttg 200  
cacgcgcctg aagcacaaaag cagatagcta ggaatgaacc atccctggga 250  
gtatgtggaa acaacggagg agctctgact tccaactgt ccatttctat 300  
gggcgaagga actgctcctg acttcagtgg ttaagggcag aattgaaaat 350  
aattctggag gaagataaga atgattcctg cgcgactgca ccgggactac 400  
aaagggcttg tcctgctggg aatcctcctg gggactctgt gggagaccgg 450  
atgcaccag atacgctatt cagttccgga agagctggag aaaggctcta 500  
gggtgggcga catctccagg gacctggggc tggagccccg ggagctcgcg 550  
gagcgcggag tccgcatcat cccagaggt aggacgcagc ttttcgcct 600







Met	Ile	Pro	Ala	Arg	Leu	His	Arg	Asp	Tyr	Lys	Gly	Leu	Val	Leu	1	5	10	15
Leu	Gly	Ile	Leu	Leu	Gly	Thr	Leu	Trp	Glu	Thr	Gly	Cys	Thr	Gln	20	25	30	
Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val	35	40	45	
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala	50	55	60	
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe	65	70	75	
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile	80	85	90	
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn	95	100	105	
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu	110	115	120	
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Glu	125	130	135	
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met	140	145	150	
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn	155	160	165	
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu	170	175	180	
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val	185	190	195	
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu	200	205	210	
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Arg	Thr	Gly	Thr	215	220	225	
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro	230	235	240	
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu	245	250	255	
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp	260	265	270	
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp	275	280	285	
Asp	Lys	Ala	Ala	Gln	Val	Phe	Lys	Leu	Asp	Cys	Asn	Ser	Gly	Thr				

TOP201-13021001



Protein Data Bank

Tyr	Leu	Val	Thr	Lys	Val	Val	Ala	Val	Asp	Arg	Asp	Ser	Gly	Gln		590	595	600
Asn	Ala	Trp	Leu	Ser	Tyr	Arg	Leu	Leu	Lys	Ala	Ser	Glu	Pro	Gly		605	610	615
Leu	Phe	Ser	Val	Gly	Leu	His	Thr	Gly	Glu	Val	Arg	Thr	Ala	Arg		620	625	630
Ala	Leu	Leu	Asp	Arg	Asp	Ala	Leu	Lys	Gln	Ser	Leu	Val	Val	Ala		635	640	645
Val	Gln	Asp	His	Gly	Gln	Pro	Pro	Leu	Ser	Ala	Thr	Val	Thr	Leu		650	655	660
Thr	Val	Ala	Val	Ala	Asp	Ser	Ile	Pro	Gln	Val	Leu	Ala	Asp	Leu		665	670	675
Gly	Ser	Leu	Glu	Ser	Pro	Ala	Asn	Ser	Glu	Thr	Ser	Asp	Leu	Thr		680	685	690
Leu	Tyr	Leu	Val	Val	Ala	Val	Ala	Ala	Val	Ser	Cys	Val	Phe	Leu		695	700	705
Ala	Phe	Val	Ile	Leu	Leu	Leu	Ala	Leu	Arg	Leu	Arg	Arg	Trp	His		710	715	720
Lys	Ser	Arg	Leu	Leu	Gln	Ala	Ser	Gly	Gly	Gly	Leu	Thr	Gly	Ala		725	730	735
Pro	Ala	Ser	His	Phe	Val	Gly	Val	Asp	Gly	Val	Gln	Ala	Phe	Leu		740	745	750
Gln	Thr	Tyr	Ser	His	Glu	Val	Ser	Leu	Thr	Thr	Asp	Ser	Arg	Lys		755	760	765
Ser	His	Leu	Ile	Phe	Pro	Gln	Pro	Asn	Tyr	Ala	Asp	Met	Leu	Val		770	775	780
Ser	Gln	Glu	Ser	Phe	Glu	Lys	Ser	Glu	Pro	Leu	Leu	Leu	Ser	Gly		785	790	795
Asp	Ser	Val	Phe	Ser	Lys	Asp	Ser	His	Gly	Leu	Ile	Glu	Val	Ser		800	805	810
Leu	Tyr	Gln	Ile	Phe	Phe	Leu	Phe	Phe	Phe	Asn	Cys	Ser	Val	Ser		815	820	825
Gln	Ala	Gly	Val	Gln	Arg	Tyr	Asp	His	Ser	Ser	Leu	Arg	Pro	Gln		830	835	840
Thr	Pro	Arg	Leu	Lys	Gln	Leu	Ser	His	Leu	Cys	Leu	Arg	Cys	Asn		845	850	855
Arg	Asp	Tyr	Arg	Cys	Lys	Pro	Pro	Thr	Val	Cys	Leu	Ser	Ile	Tyr		860	865	870
Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Leu	Leu				

875

880

885

Ser Cys Thr Asp Gly Ser Leu Thr Pro Val Ile Pro Val Leu Trp  
890 895 900

Glu Ala Glu Ala Gly Gly Ser Pro Glu Val Gly Ser Leu Arg Pro  
905 910 915

Ala

&lt;210&gt; 391

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 391

tccgtctctg tgaaccgccc cac 23

&lt;210&gt; 392

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 392

ctcgggcgca ttgtcgttct ggtc 24

&lt;210&gt; 393

&lt;211&gt; 40

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 393

ccgactgtga aagagaacgc cccagatcca cttgttcccc 40

&lt;210&gt; 394

&lt;211&gt; 999

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 394

cccaggctct agtgcaggag gagaaggagg aggagcagga ggtggagatt 50

cccagttaaa aggctccaga atcgtgtacc aggagagaa ctgaagtact 100

ggggcctcct ccaactgggtc cgaatcagta ggtgaccccg cccttgatt 150

ctggaagacc tcaccatggg acgccccga cctcgtgcgg ccaagacgtg 200

gatgttcctg ctcttgctgg ggggagcctg ggcaggacac tccagggcac 250  
aggaggacaa ggtgctgggg ggtcatgagt gccaacccca ttcgcagcct 300  
tggcaggcgg ccttggtcca gggccagcaa ctactctgtg gcggtgtcct 350  
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acacagtacg cctgggagac cacagcctac agaataaaga tggcccagag 450  
caagaataac ctgtggttca gtccatccca caccctgtct acaacagcag 500  
cgatgtggag gaccacaacc atgatctgat gcttcttcaa ctgcgtgacc 550  
aggcatccct ggggtccaaa gtgaagccca tcagcctggc agatcattgc 600  
accagcctg gccagaagtg caccgtctca ggctggggca ctgtcaccag 650  
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ttccccagaa gaagtgtgag gatgcttacc cggggcagat cacagatggc 750  
atggtctgtg caggcagcag caaaggggct gacacgtgcc agggcgattc 800  
tggaggcccc ctggtgtgtg atggtgcaact ccagggcata acatcctggg 850  
gctcagaccc ctgtgggagg tccgacaaac ctggcgtcta taccaacata 900  
tgccgctacc tggactggat caagaagatc ataggcagca agggctgatt 950  
ctaggataag cactagatct cccttaataa actcacaact ctctggttc 999

<210> 395

<211> 260

<212> PRT

<213> Homo sapiens

<400> 395

Met	Gly	Arg	Pro	Arg	Pro	Arg	Ala	Ala	Lys	Thr	Trp	Met	Phe	Leu
1				5					10					15
Leu	Leu	Leu	Gly	Gly	Ala	Trp	Ala	Gly	His	Ser	Arg	Ala	Gln	Glu
			20						25					30
Asp	Lys	Val	Leu	Gly	Gly	His	Glu	Cys	Gln	Pro	His	Ser	Gln	Pro
			35						40					45
Trp	Gln	Ala	Ala	Leu	Phe	Gln	Gly	Gln	Gln	Leu	Leu	Cys	Gly	Gly
			50						55					60
Val	Leu	Val	Gly	Gly	Asn	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Lys
			65						70					75
Lys	Pro	Lys	Tyr	Thr	Val	Arg	Leu	Gly	Asp	His	Ser	Leu	Gln	Asn
			80						85					90
Lys	Asp	Gly	Pro	Glu	Gln	Glu	Ile	Pro	Val	Val	Gln	Ser	Ile	Pro
			95						100					105

His Pro Cys Tyr Asn Ser Ser Asp Val Glu Asp His Asn His Asp  
 110 115 120  
 Leu Met Leu Leu Gln Leu Arg Asp Gln Ala Ser Leu Gly Ser Lys  
 125 130 135  
 Val Lys Pro Ile Ser Leu Ala Asp His Cys Thr Gln Pro Gly Gln  
 140 145 150  
 Lys Cys Thr Val Ser Gly Trp Gly Thr Val Thr Ser Pro Arg Glu  
 155 160 165  
 Asn Phe Pro Asp Thr Leu Asn Cys Ala Glu Val Lys Ile Phe Pro  
 170 175 180  
 Gln Lys Lys Cys Glu Asp Ala Tyr Pro Gly Gln Ile Thr Asp Gly  
 185 190 195  
 Met Val Cys Ala Gly Ser Ser Lys Gly Ala Asp Thr Cys Gln Gly  
 200 205 210  
 Asp Ser Gly Gly Pro Leu Val Cys Asp Gly Ala Leu Gln Gly Ile  
 215 220 225  
 Thr Ser Trp Gly Ser Asp Pro Cys Gly Arg Ser Asp Lys Pro Gly  
 230 235 240  
 Val Tyr Thr Asn Ile Cys Arg Tyr Leu Asp Trp Ile Lys Lys Ile  
 245 250 255  
 Ile Gly Ser Lys Gly  
 260

<210> 396

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 396

cagcctacag aataaagatg gcc 24

<210> 397

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 397

ggtgcaatga tctgccaggc tgat 24

<210> 398

<211> 48

<212> DNA









320	325	330
Gly Leu Pro Lys Cys Cys Gln Pro Asp	Ala Ala Asp Lys Ala Ser	
335	340	345
Val Leu Glu Pro Gly Arg Pro Ala Ser	Ala Gly Asn Ala Leu Lys	
350	355	360
Gly Arg Val Pro Pro Gly Asp Ser Pro	Pro Gly Asn Gly Ser Gly	
365	370	375
Pro Arg His Ile Asn Asp Ser Pro Phe	Gly Thr Leu Pro Gly Ser	
380	385	390
Ala Glu Pro Pro Leu Thr Ala Val Arg	Pro Glu Gly Ser Glu Pro	
395	400	405
Pro Gly Phe Pro Thr Ser Gly Pro Arg	Arg Arg Pro Gly Cys Ser	
410	415	420
Arg Lys Asn Arg Thr Arg Ser His Cys	Arg Leu Gly Gln Ala Gly	
425	430	435
Ser Gly Gly Gly Gly Thr Gly Asp Ser	Glu Gly Ser Gly Ala Leu	
440	445	450
Pro Ser Leu Thr Cys Ser Leu Thr Pro	Leu Gly Leu Ala Leu Val	
455	460	465
Leu Trp Thr Val Leu Gly Pro Cys		
470		

<210> 401

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 401

tggtgcct gcagtacctc tacc 24

<210> 402

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 402

ccctgcaggt cattggcagc tagg 24

<210> 403

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

aggcactgcc tgatgacacc ttccgcgacc tgggcaacct cacac 45

<210> 404

<211> 2738

<212> DNA

<213> Homo sapiens

<400> 404

ggaagtccac ggggagcttg gatgccaaag ggaggacggc tgggtcctct 50

ggagaggact actcactggc atattttctga ggtatctgta gaataaccac 100

agcctcagat actggggact ttacagtccc acagaaccgt cctcccagga 150

agctgaatcc agcaagaaca atggaggcca gcgggaagct catttgaga 200

caaaggcaag tccttttttc ctttctcctt ttgggcttat ctctggcggg 250

cgcggcggaa cctagaagct attctgtggt ggaggaaact gagggcagct 300

cctttgtcac caatttagca aaggacctgg gtctggagca gagggaattc 350

tccaggcggg gggttagggt tgtttccaga gggaacaaac tacatttgca 400

gctcaatcag gagaccgcgg atttgttgct aaatgagaaa ttggaccgtg 450

aggatctgtg cggtcacaca gagccctgtg tgctacgttt ccaagtgttg 500

ctagagagtc ccttcgagtt ttttcaagct gagctgcaag taatagacat 550

aaacgaccac tctccagtat ttctggacaa acaaagtgtg gtgaaagtat 600

cagagagcag tcctcctggg actacgtttc ctctgaagaa tgccgaagac 650

ttagatgtag gccaaaacaa tattgagaac tatataatca gcccactc 700

ctattttcgg gtcctcacc gcaaacgcag tgatggcagg aaatacccag 750

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tcaggtctac atcgaagtcc tggatgtcaa cgataatgcc cctgaatttg 900

agcagccttt ctatagagtg cagatctctg aggacagtcc ggtaggcttc 950

ctggttgtga aggtctctgc cacggatgta gacacaggag tcaacggaga 1000

gatttcctat tcacttttcc aagcttcaga agagattggc aaaaccttta 1050

agatcaatcc cttgacagga gaaattgaac taaaaaaca actcgatttc 1100

gaaaaacttc agtcctatga agtcaatatt gaggcaagag atgctggaac 1150

Sequence: 1800000

cttttctgga aaatgcacog ttctgattca agtgatagat gtgaacgacc 1200  
 atgccccaga agttaccatg tctgcattta ccagcccaat acctgagaac 1250  
 gcgcctgaaa ctgtggttgc acttttcagt gtttcagatc ttgattcagg 1300  
 agaaaatggg aaaattagtt gctccattca ggaggatcta ccttctctcc 1350  
 tgaaatccgc ggaaaacttt tacaccctac taacggagag accactagac 1400  
 agagaaagca gagcggaata caacatcact atcactgtca ctgacttggt 1450  
 gaccctatg ctgataacac agctcaatat gaccgtgctg atcgccgatg 1500  
 tcaatgacaa cgctcccgcc ttcacccaaa cctcctacac cctgttcgtc 1550  
 gcgcgagaaca acagccccgc cctgcacatc cgcagcgtca gcgctacaga 1600  
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 aggcgctggt gcgcgtggtg gtgctggacg ccaacgacaa ctgcccttc 1850  
 gtgctgtacc cgctgcagaa cggctccgcg cctgcaccg agctggtgcc 1900  
 ccgggcggcc gagccgggct acctggtgac caaggtggtg gcggtggacg 1950  
 gcgactcggg ccagaacgcc tggctgtcgt accagctgct caaggccacg 2000  
 gagctcggtc tgttcggcgt gtgggcgcac aatggcgagg tgcgcaccgc 2050  
 caggctgctg agcgagcgcg acgcggccaa gcacaggctg gtggtgctgg 2100  
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<210> 405  
 <211> 798  
 <212> PRT  
 <213> Homo sapiens

<400> 405

Met Glu Ala Ser Gly Lys Leu Ile Cys Arg Gln Arg Gln Val Leu  
 1 5 10 15

Phe Ser Phe Leu Leu Leu Gly Leu Ser Leu Ala Gly Ala Ala Glu  
 20 25 30

Pro Arg Ser Tyr Ser Val Val Glu Glu Thr Glu Gly Ser Ser Phe  
 35 40 45

Val Thr Asn Leu Ala Lys Asp Leu Gly Leu Glu Gln Arg Glu Phe  
 50 55 60

Ser Arg Arg Gly Val Arg Val Val Ser Arg Gly Asn Lys Leu His  
 65 70 75

Leu Gln Leu Asn Gln Glu Thr Ala Asp Leu Leu Leu Asn Glu Lys  
 80 85 90

Leu Asp Arg Glu Asp Leu Cys Gly His Thr Glu Pro Cys Val Leu  
 95 100 105

Arg Phe Gln Val Leu Leu Glu Ser Pro Phe Glu Phe Phe Gln Ala  
 110 115 120

Glu Leu Gln Val Ile Asp Ile Asn Asp His Ser Pro Val Phe Leu  
 125 130 135

Asp Lys Gln Met Leu Val Lys Val Ser Glu Ser Ser Pro Pro Gly  
 140 145 150

Thr Thr Phe Pro Leu Lys Asn Ala Glu Asp Leu Asp Val Gly Gln  
 155 160 165

Asn Asn Ile Glu Asn Tyr Ile Ile Ser Pro Asn Ser Tyr Phe Arg  
 170 175 180

Val Leu Thr Arg Lys Arg Ser Asp Gly Arg Lys Tyr Pro Glu Leu  
 185 190 195

Val Leu Asp Lys Ala Leu Asp Arg Glu Glu Glu Ala Glu Leu Arg  
 200 205 210

Leu Thr Leu Thr Ala Leu Asp Gly Gly Ser Pro Pro Arg Ser Gly  
 215 220 225

Thr Ala Gln Val Tyr Ile Glu Val Leu Asp Val Asn Asp Asn Ala

CONCOT = 1800-1000

230	235	240
Pro Glu Phe Glu Gln Pro Phe Tyr Arg	Val Gln Ile Ser Glu Asp	
245	250	255
Ser Pro Val Gly Phe Leu Val Val Lys	Val Ser Ala Thr Asp Val	
260	265	270
Asp Thr Gly Val Asn Gly Glu Ile Ser	Tyr Ser Leu Phe Gln Ala	
275	280	285
Ser Glu Glu Ile Gly Lys Thr Phe Lys	Ile Asn Pro Leu Thr Gly	
290	295	300
Glu Ile Glu Leu Lys Lys Gln Leu Asp	Phe Glu Lys Leu Gln Ser	
305	310	315
Tyr Glu Val Asn Ile Glu Ala Arg Asp	Ala Gly Thr Phe Ser Gly	
320	325	330
Lys Cys Thr Val Leu Ile Gln Val Ile	Asp Val Asn Asp His Ala	
335	340	345
Pro Glu Val Thr Met Ser Ala Phe Thr	Ser Pro Ile Pro Glu Asn	
350	355	360
Ala Pro Glu Thr Val Val Ala Leu Phe	Ser Val Ser Asp Leu Asp	
365	370	375
Ser Gly Glu Asn Gly Lys Ile Ser Cys	Ser Ile Gln Glu Asp Leu	
380	385	390
Pro Phe Leu Leu Lys Ser Ala Glu Asn	Phe Tyr Thr Leu Leu Thr	
395	400	405
Glu Arg Pro Leu Asp Arg Glu Ser Arg	Ala Glu Tyr Asn Ile Thr	
410	415	420
Ile Thr Val Thr Asp Leu Gly Thr Pro	Met Leu Ile Thr Gln Leu	
425	430	435
Asn Met Thr Val Leu Ile Ala Asp Val	Asn Asp Asn Ala Pro Ala	
440	445	450
Phe Thr Gln Thr Ser Tyr Thr Leu Phe	Val Arg Glu Asn Asn Ser	
455	460	465
Pro Ala Leu His Ile Arg Ser Val Ser	Ala Thr Asp Arg Asp Ser	
470	475	480
Gly Thr Asn Ala Gln Val Thr Tyr Ser	Leu Leu Pro Pro Gln Asp	
485	490	495
Pro His Leu Pro Leu Thr Ser Leu Val	Ser Ile Asn Ala Asp Asn	
500	505	510
Gly His Leu Phe Ala Leu Arg Ser Leu	Asp Tyr Glu Ala Leu Gln	
515	520	525



Gly	Phe	Gln	Phe	Arg	Val	Gly	Ala	Ser	Asp	His	Gly	Ser	Pro	Ala	
				530					535					540	
Leu	Ser	Ser	Glu	Ala	Leu	Val	Arg	Val	Val	Val	Leu	Asp	Ala	Asn	
				545					550					555	
Asp	Asn	Ser	Pro	Phe	Val	Leu	Tyr	Pro	Leu	Gln	Asn	Gly	Ser	Ala	
				560					565					570	
Pro	Cys	Thr	Glu	Leu	Val	Pro	Arg	Ala	Ala	Glu	Pro	Gly	Tyr	Leu	
				575					580					585	
Val	Thr	Lys	Val	Val	Ala	Val	Asp	Gly	Asp	Ser	Gly	Gln	Asn	Ala	
				590					595					600	
Trp	Leu	Ser	Tyr	Gln	Leu	Leu	Lys	Ala	Thr	Glu	Leu	Gly	Leu	Phe	
				605					610					615	
Gly	Val	Trp	Ala	His	Asn	Gly	Glu	Val	Arg	Thr	Ala	Arg	Leu	Leu	
				620					625					630	
Ser	Glu	Arg	Asp	Ala	Ala	Lys	His	Arg	Leu	Val	Val	Leu	Val	Lys	
				635					640					645	
Asp	Asn	Gly	Glu	Pro	Pro	Arg	Ser	Ala	Thr	Ala	Thr	Leu	His	Val	
				650					655					660	
Leu	Leu	Val	Asp	Gly	Phe	Ser	Gln	Pro	Tyr	Leu	Pro	Leu	Pro	Glu	
				665					670					675	
Ala	Ala	Pro	Thr	Gln	Ala	Gln	Ala	Asp	Leu	Leu	Thr	Val	Tyr	Leu	
				680					685					690	
Val	Val	Ala	Leu	Ala	Ser	Val	Ser	Ser	Leu	Phe	Leu	Phe	Ser	Val	
				695					700					705	
Leu	Leu	Phe	Val	Ala	Val	Arg	Leu	Cys	Arg	Arg	Ser	Arg	Ala	Ala	
				710					715					720	
Ser	Val	Gly	Arg	Cys	Leu	Val	Pro	Glu	Gly	Pro	Leu	Pro	Gly	His	
				725					730					735	
Leu	Val	Asp	Met	Ser	Gly	Thr	Arg	Thr	Leu	Ser	Gln	Ser	Tyr	Gln	
				740					745					750	
Tyr	Glu	Val	Cys	Leu	Ala	Gly	Gly	Ser	Gly	Thr	Asn	Glu	Phe	Lys	
				755					760					765	
Phe	Leu	Lys	Pro	Ile	Ile	Pro	Asn	Phe	Pro	Pro	Gln	Cys	Pro	Gly	
				770					775					780	
Lys	Glu	Ile	Gln	Gly	Asn	Ser	Thr	Phe	Pro	Asn	Asn	Phe	Gly	Phe	
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Asn Ile Gln

<210> 406

<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 406  
ctgagaacgc gcctgaaact gtg 23

<210> 407  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 407  
agcgttgtca ttgacatcgg cg 22

<210> 408  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 408  
ttagtgtgtc cattcaggag gatctaccct tcctcctgaa atccgcggaa 50

<210> 409  
<211> 1379  
<212> DNA  
<213> Homo sapiens

<400> 409  
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cggtcgacga ccgccccgcg tcattcggct cctcggctgg tggcaagtat 150  
tgctgtgggt gctgggactt cccgtccgcg gcgtggaggt tgcagaggaa 200  
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gagttcagag cctagcggcg tcacctgtgg tgctggagga gcggaggact 450  
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 aaccaatggc cagatttaat catacagatc gaacactgga aacactgaaa 950  
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 aactcaagcc gaccaaataag gccctcttcc cagcactttg ataaaaagt 1050  
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 ttcaatcctt cgtttcagaa attagtgcga cagtttcata cattttctcc 1250  
 agtgacgtgt tgacttgaaa cttcaggcag attaaaagaa tcatttggtg 1300  
 aacaactgaa tgtataaaaa aattataaac tgggtgttta actagtattg 1350  
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<210> 410  
 <211> 360  
 <212> PRT  
 <213> Homo sapiens

<400> 410  
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 20 25 30  
 Arg Gly Val Glu Val Ala Glu Glu Ser Gly Arg Leu Trp Ser Glu  
 35 40 45  
 Glu Gln Pro Ala His Pro Leu Gln Val Gly Ala Val Tyr Leu Gly  
 50 55 60  
 Glu Glu Glu Leu Leu His Asp Pro Met Gly Gln Asp Arg Ala Ala  
 65 70 75  
 Glu Glu Ala Asn Ala Val Leu Gly Leu Asp Thr Gln Gly Asp His

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Met	Val	Met	Leu	Ser	Val	Ile	Pro	Gly	Glu	Ala	Glu	Asp	Lys	Val	
				95					100					105	
Ser	Ser	Glu	Pro	Ser	Gly	Val	Thr	Cys	Gly	Ala	Gly	Gly	Ala	Glu	
				110					115					120	
Asp	Ser	Arg	Cys	Asn	Val	Arg	Glu	Ser	Leu	Phe	Ser	Leu	Asp	Gly	
				125					130					135	
Ala	Gly	Ala	His	Phe	Pro	Asp	Arg	Glu	Glu	Glu	Tyr	Tyr	Thr	Glu	
				140					145					150	
Pro	Glu	Val	Ala	Glu	Ser	Asp	Ala	Ala	Pro	Thr	Glu	Asp	Ser	Asn	
				155					160					165	
Asn	Thr	Glu	Ser	Leu	Lys	Ser	Pro	Lys	Val	Asn	Cys	Glu	Glu	Arg	
				170					175					180	
Asn	Ile	Thr	Gly	Leu	Glu	Asn	Phe	Thr	Leu	Lys	Ile	Leu	Asn	Met	
				185					190					195	
Ser	Gln	Asp	Leu	Met	Asp	Phe	Leu	Asn	Pro	Asn	Gly	Ser	Asp	Cys	
				200					205					210	
Thr	Leu	Val	Leu	Phe	Tyr	Thr	Pro	Trp	Cys	Arg	Phe	Ser	Ala	Ser	
				215					220					225	
Leu	Ala	Pro	His	Phe	Asn	Ser	Leu	Pro	Arg	Ala	Phe	Pro	Ala	Leu	
				230					235					240	
His	Phe	Leu	Ala	Leu	Asp	Ala	Ser	Gln	His	Ser	Ser	Leu	Ser	Thr	
				245					250					255	
Arg	Phe	Gly	Thr	Val	Ala	Val	Pro	Asn	Ile	Leu	Leu	Phe	Gln	Gly	
				260					265					270	
Ala	Lys	Pro	Met	Ala	Arg	Phe	Asn	His	Thr	Asp	Arg	Thr	Leu	Glu	
				275					280					285	
Thr	Leu	Lys	Ile	Phe	Ile	Phe	Asn	Gln	Thr	Gly	Ile	Glu	Ala	Lys	
				290					295					300	
Lys	Asn	Val	Val	Val	Thr	Gln	Ala	Asp	Gln	Ile	Gly	Pro	Leu	Pro	
				305					310					315	
Ser	Thr	Leu	Ile	Lys	Ser	Val	Asp	Trp	Leu	Leu	Val	Phe	Ser	Leu	
				320					325					330	
Phe	Phe	Leu	Ile	Ser	Phe	Ile	Met	Tyr	Ala	Thr	Ile	Arg	Thr	Glu	
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Ser	Ile	Arg	Trp	Leu	Ile	Pro	Gly	Gln	Glu	Gln	Glu	His	Val	Glu	
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<210> 411  
 <211> 24

<212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic oligonucleotide probe

<400> 411  
 cacagagcca gaagtggcgg aatc 24

<210> 412  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 412  
 ccacatgttc ctgctcttgt cctgg 25

<210> 413  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 413  
 cggtagtgac tgtactctag tcctgtttta caccocgtgg tgccg 45

<210> 414  
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 <212> DNA  
 <213> Homo sapiens

<400> 414  
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 ggctcggcgc gcggtctctt cctctttggc cagcccgact tctcctacaa 150  
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 tcgaatacca gaacatgcgg ctgccaacc tgctgggcca cgagaccatg 250  
 aaggaggtgc tggagcaggc cggcgttgg atcccgctgg tcatgaagca 300  
 gtgccaccgc gacaccaaga agttcctgtg ctgcctcttc gccccgtct 350  
 gcctcgatga cctagacgag accatccagc catgccactc gctctgcgtg 400  
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 gcccgacatg cttgagtgcg accgtttccc ccaggacaac gacctttgca 500  
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taacctacat caaccgagat accaaaatca tcctggagac caagagcaag 700  
accatttaca agctgaacgg tgtgtccgaa agggacctga agaaatcgg 750  
gctgtggctc aaagacagct tgcagtgcac ctgtgaggag atgaacgaca 800  
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gaatcttgta gaaatattca aactaataaa atcatgaata ttttaa 1196

<210> 415

<211> 295

<212> PRT

<213> Homo sapiens

<400> 415

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His	Cys	Cys	Leu	Gly	Ser	Ala	Arg	Gly	Leu	Phe	Leu	Phe	Gly	Gln	20	25	30	
Pro	Asp	Phe	Ser	Tyr	Lys	Arg	Ser	Asn	Cys	Lys	Pro	Ile	Pro	Val	35	40	45	
Asn	Leu	Gln	Leu	Cys	His	Gly	Ile	Glu	Tyr	Gln	Asn	Met	Arg	Leu	50	55	60	
Pro	Asn	Leu	Leu	Gly	His	Glu	Thr	Met	Lys	Glu	Val	Leu	Glu	Gln	65	70	75	
Ala	Gly	Ala	Trp	Ile	Pro	Leu	Val	Met	Lys	Gln	Cys	His	Pro	Asp	80	85	90	
Thr	Lys	Lys	Phe	Leu	Cys	Ser	Leu	Phe	Ala	Pro	Val	Cys	Leu	Asp	95	100	105	
Asp	Leu	Asp	Glu	Thr	Ile	Gln	Pro	Cys	His	Ser	Leu	Cys	Val	Gln	110	115	120	
Val	Lys	Asp	Arg	Cys	Ala	Pro	Val	Met	Ser	Ala	Phe	Gly	Phe	Pro	125	130	135	



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 418

ctcttcctct ttggccagcc cgacttctcc tacaagcgca gaattgc 47

<210> 419

<211> 1830

<212> DNA

<213> Homo sapiens

<400> 419

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ccgtgcggcg accatcctgg gtgcgtggct gaactttgcc gggagtgtgc 350

tacgcatggt gccctgcatg gttgttggga cccaaaaccc atttgccttc 400

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ctctccagcc aagctggctg ccttgtggtt ccagagcac cagcagacca 500

cggccaacat gctcgccacc atgtcgaacc ctctgggcgt ccttgtggcc 550

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gaacaaggcc tatgtcatcc tggctgtgtg cttgggggga atgatcgga 800

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ccctttgccc tgggtgtcca gctgcaggga cagacccttg ccctggctgc 1050

cacctgctcg ctgctcgggc tgtttggctt ctcggtgggc ccctggcca 1100

the "root" of the tree



tggagttggc ggtcgagtgt tccttccccg tgggggaggg ggctgccaca 1150  
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 aatgacggca ctgactgtgc gacgctcgga gccgtccttg tccacctgcc 1250  
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<210> 420

<211> 560

<212> PRT

<213> Homo sapiens

<400> 420

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Val Phe Leu Leu Ala Ile Ser Leu Leu Asn Cys Ser Asn Ala Thr  
 35 40 45

Leu Trp Leu Ser Phe Ala Pro Val Ala Asp Val Ile Ala Glu Asp  
 50 55 60

Leu Val Leu Ser Met Glu Gln Ile Asn Trp Leu Ser Leu Val Tyr  
 65 70 75

Leu Val Val Ser Thr Pro Phe Gly Val Ala Ala Ile Trp Ile Leu  
 80 85 90

Asp Ser Val Gly Leu Arg Ala Ala Thr Ile Leu Gly Ala Trp Leu  
 95 100 105

Asn Phe Ala Gly Ser Val Leu Arg Met Val Pro Cys Met Val Val



Pro Ser Leu Ser Thr Cys Gln Gln Gly Glu Asp Pro Leu Asp Trp  
410 415 420

Thr Val Ser Leu Leu Leu Met Ala Gly Leu Cys Thr Phe Phe Ser  
425 430 435

Cys Ile Leu Ala Val Phe Phe His Thr Pro Tyr Arg Arg Leu Gln  
440 445 450

Ala Glu Ser Gly Glu Pro Pro Ser Thr Arg Asn Ala Val Gly Gly  
455 460 465

Ala Asp Ser Gly Pro Gly Val Asp Arg Gly Gly Ala Gly Arg Ala  
470 475 480

Gly Val Leu Gly Pro Ser Thr Ala Thr Pro Glu Cys Thr Ala Arg  
485 490 495

Gly Ala Ser Leu Glu Asp Pro Arg Gly Pro Gly Ser Pro His Pro  
500 505 510

Ala Cys His Arg Ala Thr Pro Arg Ala Gln Gly Pro Ala Ala Thr  
515 520 525

Asp Ala Pro Ser Arg Pro Gly Arg Leu Ala Gly Arg Val Gln Ala  
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Ser Arg Phe Ile Asp Pro Ala Gly Ser His Ser Ser Phe Ser Ser  
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Pro Trp Val Ile Thr  
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<210> 421

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 421

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<210> 422

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 422

cgggtcaata aacctggacg cttgg 25

<210> 423

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 424

<211> 4313

<212> DNA

<213> Homo sapiens

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tggcaattct tgatcggcgt ttggacatct cagatcgctt ccaatgaaga 150  
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<210> 425
<211> 1184
<212> PRT
<213> Homo sapiens
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<400> 425

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				20					25						
Thr	Val	Lys	Tyr	Gln	Val	Ser	Glu	Glu	Val	Pro	Ser	Gly	Thr	Val	45
				35					40						
Ile	Gly	Lys	Leu	Ser	Gln	Glu	Leu	Gly	Arg	Glu	Glu	Arg	Arg	Arg	60
				50					55						
Gln	Ala	Gly	Ala	Ala	Phe	Gln	Val	Leu	Gln	Leu	Pro	Gln	Ala	Leu	75
				65					70						
Pro	Ile	Gln	Val	Asp	Ser	Glu	Glu	Gly	Leu	Leu	Ser	Thr	Gly	Arg	90
				80					85						
Arg	Leu	Asp	Arg	Glu	Gln	Leu	Cys	Arg	Gln	Trp	Asp	Pro	Cys	Leu	105
				95					100						
Val	Ser	Phe	Asp	Val	Leu	Ala	Thr	Gly	Asp	Leu	Ala	Leu	Ile	His	120
				110					115						
Val	Glu	Ile	Gln	Val	Leu	Asp	Ile	Asn	Asp	His	Gln	Pro	Arg	Phe	135
				125					130						
Pro	Lys	Gly	Glu	Gln	Glu	Leu	Glu	Ile	Ser	Glu	Ser	Ala	Ser	Leu	150
				140					145						
Arg	Thr	Arg	Ile	Pro	Leu	Asp	Arg	Ala	Leu	Asp	Pro	Asp	Thr	Gly	165
				155					160						
Pro	Asn	Thr	Leu	His	Thr	Tyr	Thr	Leu	Ser	Pro	Ser	Glu	His	Phe	180
				170					175						
Ala	Leu	Asp	Val	Ile	Val	Gly	Pro	Asp	Glu	Thr	Lys	His	Ala	Glu	195
				185					190						

101201-180200

Leu Ile Val Val Lys Glu Leu Asp Arg Glu Ile His Ser Phe Phe  
200 205 210

Asp Leu Val Leu Thr Ala Tyr Asp Asn Gly Asn Pro Pro Lys Ser  
215 220 225

Gly Thr Ser Leu Val Lys Val Asn Val Leu Asp Ser Asn Asp Asn  
230 235 240

Ser Pro Ala Phe Ala Glu Ser Ser Leu Ala Leu Glu Ile Gln Glu  
245 250 255

Asp Ala Ala Pro Gly Thr Leu Leu Ile Lys Leu Thr Ala Thr Asp  
260 265 270

Pro Asp Gln Gly Pro Asn Gly Glu Val Glu Phe Phe Leu Ser Lys  
275 280 285

His Met Pro Pro Glu Val Leu Asp Thr Phe Ser Ile Asp Ala Lys  
290 295 300

Thr Gly Gln Val Ile Leu Arg Arg Pro Leu Asp Tyr Glu Lys Asn  
305 310 315

Pro Ala Tyr Glu Val Asp Val Gln Ala Arg Asp Leu Gly Pro Asn  
320 325 330

Pro Ile Pro Ala His Cys Lys Val Leu Ile Lys Val Leu Asp Val  
335 340 345

Asn Asp Asn Ile Pro Ser Ile His Val Thr Trp Ala Ser Gln Pro  
350 355 360

Ser Leu Val Ser Glu Ala Leu Pro Lys Asp Ser Phe Ile Ala Leu  
365 370 375

Val Met Ala Asp Asp Leu Asp Ser Gly His Asn Gly Leu Val His  
380 385 390

Cys Trp Leu Ser Gln Glu Leu Gly His Phe Arg Leu Lys Arg Thr  
395 400 405

Asn Gly Asn Thr Tyr Met Leu Leu Thr Asn Ala Thr Leu Asp Arg  
410 415 420

Glu Gln Trp Pro Lys Tyr Thr Leu Thr Leu Leu Ala Gln Asp Gln  
425 430 435

Gly Leu Gln Pro Leu Ser Ala Lys Lys Gln Leu Ser Ile Gln Ile  
440 445 450

Ser Asp Ile Asn Asp Asn Ala Pro Val Phe Glu Lys Ser Arg Tyr  
455 460 465

Glu Val Ser Thr Arg Glu Asn Asn Leu Pro Ser Leu His Leu Ile  
470 475 480

Thr Ile Lys Ala His Asp Ala Asp Leu Gly Ile Asn Gly Lys Val



	485	490	495
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Asp Ser Asn Thr	Gly Glu Val Thr Ala	Gln Arg Ser Leu Asn	Tyr
	515	520	525
Glu Glu Met Ala	Gly Phe Glu Phe Gln	Val Ile Ala Glu Asp	Ser
	530	535	540
Gly Gln Pro Met	Leu Ala Ser Ser Val	Ser Val Trp Val Ser	Leu
	545	550	555
Leu Asp Ala Asn	Asp Asn Ala Pro Glu	Val Val Gln Pro Val	Leu
	560	565	570
Ser Asp Gly Lys	Ala Ser Leu Ser Val	Leu Val Asn Ala Ser	Thr
	575	580	585
Gly His Leu Leu	Val Pro Ile Glu Thr	Pro Asn Gly Leu Gly	Pro
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Ala Gly Thr Asp	Thr Pro Pro Leu Ala	Thr His Ser Ser Arg	Pro
	605	610	615
Phe Leu Leu Thr	Thr Ile Val Ala Arg	Asp Ala Asp Ser Gly	Ala
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Asn Gly Glu Pro	Leu Tyr Ser Ile Arg	Asn Gly Asn Glu Ala	His
	635	640	645
Leu Phe Ile Leu	Asn Pro His Thr Gly	Gln Leu Phe Val Asn	Val
	650	655	660
Thr Asn Ala Ser	Ser Leu Ile Gly Ser	Glu Trp Glu Leu Glu	Ile
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Val Val Glu Asp	Gln Gly Ser Pro Pro	Leu Gln Thr Arg Ala	Leu
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Leu Arg Val Met	Phe Val Thr Ser Val	Asp His Leu Arg Asp	Ser
	695	700	705
Ala Arg Lys Pro	Gly Ala Leu Ser Met	Ser Met Leu Thr Val	Ile
	710	715	720
Cys Leu Ala Val	Leu Leu Gly Ile Phe	Gly Leu Ile Leu Ala	Leu
	725	730	735
Phe Met Ser Ile	Cys Arg Thr Glu Lys	Lys Asp Asn Arg Ala	Tyr
	740	745	750
Asn Cys Arg Glu	Ala Glu Ser Thr Tyr	Arg Gln Gln Pro Lys	Arg
	755	760	765
Pro Gln Lys His	Ile Gln Lys Ala Asp	Ile His Leu Val Pro	Val
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 815 820 825  
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 Val Leu Gln Asp Thr Val Asn Leu Leu Phe Asn His Pro Arg Gln  
 845 850 855  
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 875 880 885  
 Pro Thr Gly Arg Leu Ala Gly Asp Gln Gly Ser Glu Glu Ala Pro  
 890 895 900  
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 920 925 930  
 Ile Leu Arg Ser Leu Val Arg Leu Ser Val Ala Ala Phe Ala Glu  
 935 940 945  
 Arg Asn Pro Val Glu Glu Leu Thr Val Asp Ser Pro Pro Val Gln  
 950 955 960  
 Gln Ile Ser Gln Leu Leu Ser Leu Leu His Gln Gly Gln Phe Gln  
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 Pro Lys Pro Asn His Arg Gly Asn Lys Tyr Leu Ala Lys Pro Gly  
 980 985 990  
 Gly Ser Arg Ser Ala Ile Pro Asp Thr Asp Gly Pro Ser Ala Arg  
 995 1000 1005  
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 1010 1015 1020  
 Pro Glu Glu Asp Leu Ser Val Lys Gln Leu Leu Glu Glu Glu Leu  
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 1055 1060 1065  
 Thr Thr Asn Tyr Arg Asp Asn Val Ile Ser Pro Asp Ala Ala Ala

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Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val		
1100	1105	1110
Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser		
1115	1120	1125
Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser		
1130	1135	1140
Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala		
1145	1150	1155
Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr Gly Thr		
1160	1165	1170
Glu Gly Lys Ser Arg Gly Ser Ser Ser Ser Ser Arg Cys Leu		
1175	1180	

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 429
<211> 2037

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<213> Homo sapiens

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tttgatttg	ggtggctttt	cttcatgcgc	caattgttta	aagactatga	250
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 <213> Homo sapiens

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 Lys Asp Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser  
 35 40 45  
 Val Thr Phe Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe  
 50 55 60  
 Glu Ile Leu Gly Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp  
 65 70 75  
 Lys Met Asn Leu Cys Val Ile Leu Leu Ile Leu Val Phe Met Val  
 80 85 90  
 Pro Phe Tyr Ile Gly Tyr Phe Ile Val Ser Asn Ile Arg Leu Leu  
 95 100 105  
 His Lys Gln Arg Leu Leu Phe Ser Cys Leu Leu Trp Leu Thr Phe  
 110 115 120

Met Tyr Phe Phe Trp Lys Leu Gly Asp Pro Phe Pro Ile Leu Ser  
125 130 135

Pro Lys His Gly Ile Leu Ser Ile Glu Gln Leu Ile Ser Arg Val  
140 145 150

Gly Val Ile Gly Val Thr Leu Met Ala Leu Leu Ser Gly Phe Gly  
155 160 165

Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr Phe Leu Arg Asn  
170 175 180

Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg Leu Leu Gln  
185 190 195

Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala Met Ala  
200 205 210

Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro Ser  
215 220 225

Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly  
230 235 240

Ser Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu  
245 250 255

Glu Leu Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala  
260 265 270

Thr Lys Glu Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr  
275 280 285

Phe Asn Phe Leu Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys  
290 295 300

Ile Phe Met Ala Thr Ile Asn Ile Val Phe Asp Arg Val Gly Lys  
305 310 315

Thr Asp Pro Val Thr Arg Gly Ile Glu Ile Thr Val Asn Tyr Leu  
320 325 330

Gly Ile Gln Phe Asp Val Lys Phe Trp Ser Gln His Ile Ser Phe  
335 340 345

Ile Leu Val Gly Ile Ile Ile Val Thr Ser Ile Arg Gly Leu Leu  
350 355 360

Ile Thr Leu Thr Lys Phe Phe Tyr Ala Ile Ser Ser Ser Lys Ser  
365 370 375

Ser Asn Val Ile Val Leu Leu Leu Ala Gln Ile Met Gly Met Tyr  
380 385 390

Phe Val Ser Ser Val Leu Leu Ile Arg Met Ser Met Pro Leu Glu  
395 400 405

Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu Leu Gln Phe Asn

410

415

420

Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val Ser Ala Leu  
425 430 435

Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala Pro Glu  
440 445 450

Lys Gln Met Ala Pro  
455

&lt;210&gt; 431

&lt;211&gt; 407

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; 78, 81, 113, 157, 224, 297

&lt;223&gt; unknown base

&lt;400&gt; 431

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tttccag 407

&lt;210&gt; 432

&lt;211&gt; 457

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; 31, 66, 81-82, 84, 122, 184, 187, 232, 241, 400, 424, 427, 434

&lt;223&gt; unknown base

&lt;400&gt; 432

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 ccataaagaa cttgatgctc cgagatgcct ccacagtgat ccagtgatg 3100

TOPIC: HBBCT

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<210> 437

<211> 1141

<212> PRT

<213> Homo sapiens

<400> 437

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Cys Tyr Leu Phe Gly Ser Leu Leu Val Glu Leu Leu Phe Ser Arg  
20 25 30

Ala Val Ala Phe Asn Leu Asp Val Met Gly Ala Leu Arg Lys Glu  
35 40 45

Gly Glu Pro Gly Ser Leu Phe Gly Phe Ser Val Ala Leu His Arg  
50 55 60

Gln Leu Gln Pro Arg Pro Gln Ser Trp Leu Leu Val Gly Ala Pro  
65 70 75

Gln Ala Leu Ala Leu Pro Gly Gln Gln Ala Asn Arg Thr Gly Gly

90

Val Tyr Leu Asn Gln Gly Gly His Trp Ala Gly Ile Ser Pro Leu  
365 370 375

302

Arg Leu Cys Gly Ser Pro Asp Ser Met Phe Gly Ile Ser Leu Ala  
380 385 390

Val Leu Gly Asp Leu Asn Gln Asp Gly Phe Pro Asp Ile Ala Val  
395 400 405

Gly Ala Pro Phe Asp Gly Asp Gly Lys Val Phe Ile Tyr His Gly  
410 415 420

Ser Ser Leu Gly Val Val Ala Lys Pro Ser Gln Val Leu Glu Gly  
425 430 435

Glu Ala Val Gly Ile Lys Ser Phe Gly Tyr Ser Leu Ser Gly Ser  
440 445 450

Leu Asp Met Asp Gly Asn Gln Tyr Pro Asp Leu Leu Val Gly Ser  
455 460 465

Leu Ala Asp Thr Ala Val Leu Phe Arg Ala Arg Pro Ile Leu His  
470 475 480

Val Ser His Glu Val Ser Ile Ala Pro Arg Ser Ile Asp Leu Glu  
485 490 495

Gln Pro Asn Cys Ala Gly Gly His Ser Val Cys Val Asp Leu Arg  
500 505 510

Val Cys Phe Ser Tyr Ile Ala Val Pro Ser Ser Tyr Ser Pro Thr  
515 520 525

Val Ala Leu Asp Tyr Val Leu Asp Ala Asp Thr Asp Arg Arg Leu  
530 535 540

Arg Gly Gln Val Pro Arg Val Thr Phe Leu Ser Arg Asn Leu Glu  
545 550 555

Glu Pro Lys His Gln Ala Ser Gly Thr Val Trp Leu Lys His Gln  
560 565 570

His Asp Arg Val Cys Gly Asp Ala Met Phe Gln Leu Gln Glu Asn  
575 580 585

Val Lys Asp Lys Leu Arg Ala Ile Val Val Thr Leu Ser Tyr Ser  
590 595 600

Leu Gln Thr Pro Arg Leu Arg Arg Gln Ala Pro Gly Gln Gly Leu  
605 610 615

Pro Pro Val Ala Pro Ile Leu Asn Ala His Gln Pro Ser Thr Gln  
620 625 630

Arg Ala Glu Ile His Phe Leu Lys Gln Gly Cys Gly Glu Asp Lys  
635 640 645

Ile Cys Gln Ser Asn Leu Gln Leu Val His Ala Arg Phe Cys Thr  
650 655 660

Arg Val Ser Asp Thr Glu Phe Gln Pro Leu Pro Met Asp Val Asp

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Gly Thr Thr Ala	Leu Phe Ala Leu Ser	Gly Gln Pro Val Ile	Gly		
	680		685		690
Leu Glu Leu Met	Val Thr Asn Leu Pro	Ser Asp Pro Ala Gln	Pro		
	695		700		705
Gln Ala Asp Gly	Asp Asp Ala His Glu	Ala Gln Leu Leu Val	Met		
	710		715		720
Leu Pro Asp Ser	Leu His Tyr Ser Gly	Val Arg Ala Leu Asp	Pro		
	725		730		735
Ala Glu Lys Pro	Leu Cys Leu Ser Asn	Glu Asn Ala Ser His	Val		
	740		745		750
Glu Cys Glu Leu	Gly Asn Pro Met Lys	Arg Gly Ala Gln Val	Thr		
	755		760		765
Phe Tyr Leu Ile	Leu Ser Thr Ser Gly	Ile Ser Ile Glu Thr	Thr		
	770		775		780
Glu Leu Glu Val	Glu Leu Leu Leu Ala	Thr Ile Ser Glu Gln	Glu		
	785		790		795
Leu His Pro Val	Ser Ala Arg Ala Arg	Val Phe Ile Glu Leu	Pro		
	800		805		810
Leu Ser Ile Ala	Gly Met Ala Ile Pro	Gln Gln Leu Phe Phe	Ser		
	815		820		825
Gly Val Val Arg	Gly Glu Arg Ala Met	Gln Ser Glu Arg Asp	Val		
	830		835		840
Gly Ser Lys Val	Lys Tyr Glu Val Thr	Val Ser Asn Gln Gly	Gln		
	845		850		855
Ser Leu Arg Thr	Leu Gly Ser Ala Phe	Leu Asn Ile Met Trp	Pro		
	860		865		870
His Glu Ile Ala	Asn Gly Lys Trp Leu	Leu Tyr Pro Met Gln	Val		
	875		880		885
Glu Leu Glu Gly	Gly Gln Gly Pro Gly	Gln Lys Gly Leu Cys	Ser		
	890		895		900
Pro Arg Pro Asn	Ile Leu His Leu Asp	Val Asp Ser Arg Asp	Arg		
	905		910		915
Arg Arg Arg Glu	Leu Glu Pro Pro Glu	Gln Gln Glu Pro Gly	Glu		
	920		925		930
Arg Gln Glu Pro	Ser Met Ser Trp Trp	Pro Val Ser Ser Ala	Glu		
	935		940		945
Lys Lys Lys Asn	Ile Thr Leu Asp Cys	Ala Arg Gly Thr Ala	Asn		
	950		955		960

Cys Val Val Phe Ser Cys Pro Leu Tyr Ser Phe Asp Arg Ala Ala	965	970	975
Val Leu His Val Trp Gly Arg Leu Trp Asn Ser Thr Phe Leu Glu	980	985	990
Glu Tyr Ser Ala Val Lys Ser Leu Glu Val Ile Val Arg Ala Asn	995	1000	1005
Ile Thr Val Lys Ser Ser Ile Lys Asn Leu Met Leu Arg Asp Ala	1010	1015	1020
Ser Thr Val Ile Pro Val Met Val Tyr Leu Asp Pro Met Ala Val	1025	1030	1035
Val Ala Glu Gly Val Pro Trp Trp Val Ile Leu Leu Ala Val Leu	1040	1045	1050
Ala Gly Leu Leu Val Leu Ala Leu Leu Val Leu Leu Leu Trp Lys	1055	1060	1065
Met Gly Phe Phe Lys Arg Ala Lys His Pro Glu Ala Thr Val Pro	1070	1075	1080
Gln Tyr His Ala Val Lys Ile Pro Arg Glu Asp Arg Gln Gln Phe	1085	1090	1095
Lys Glu Glu Lys Thr Gly Thr Ile Leu Arg Asn Asn Trp Gly Ser	1100	1105	1110
Pro Arg Arg Glu Gly Pro Asp Ala His Pro Ile Leu Ala Ala Asp	1115	1120	1125
Gly His Pro Glu Leu Gly Pro Asp Gly His Pro Gly Pro Gly Thr	1130	1135	1140

Ala

<210> 438

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 438

ggctgacacc gcagtgtct tcag 24

<210> 439

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 439  
gctgctgggg actgcaatgt agct 24

<210> 440

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 440

catcctccat gtctcccatg aggtctctat tgctccacga agcatc 46

<210> 441

<211> 1964

<212> DNA

<213> Homo sapiens

<400> 441

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agcagctcca gaaagcagcg agttggcaga gcagggctgc atttccagca 100

ggagctgcga gcacagtgtt ggctcacaac aagatgtctc aggtgtcagc 150

cgtactgtgt gtgtgtgcag ccgcttggtg cagtcagtct ctgcagctg 200

ccgcggcggt ggctgcagcc ggggggcggt cggacggcgg taattttctg 250

gatgataaac aatggctcac cacaatctct cagtatgaca aggaagtcgg 300

acagtggaac aaattccgag acgaagtaga ggatgattat ttccgcactt 350

ggagtccagg aaaacccttc gatcaggctt tagatccagc taaggatcca 400

tgcttaaaga tgaaatgtag tcgccataaa gtatgcattg ctcaagattc 450

tcagactgca gtctgcatta gtcaccggag gcttacacac aggatgaaag 500

aagcaggagt agaccatagg cagtggaggg gtcccatatt atccacctgc 550

aagcagtgcc cagtgttcta tcccagccct gtttgtgggt cagatgggtca 600

tacctactct ttccagtgc aactagaata tcaggcatgt gtcttaggaa 650

aacagatctc agtcaaatgt gaaggacatt gcccatgtcc ttcagataag 700

cccaccagta caagcagaaa tgtaagaga gcatgcagt acctggagtt 750

caggggaagt gcaaacagat tgcgggactg gttcaaggcc cttcatgaaa 800

gtggaagtca aaacaagaag acaaaaacat tgctgaggcc tgagagaagc 850

agattcgata ccagcatctt gccaatgtgc aaggactcac ttggctggat 900

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TOH20T-H3DCT00T

Phe Arg Asp Glu Val Glu Asp Asp Tyr	Phe Arg Thr Trp Ser Pro
65	70 75
Gly Lys Pro Phe Asp Gln Ala Leu Asp	Pro Ala Lys Asp Pro Cys
80	85 90
Leu Lys Met Lys Cys Ser Arg His Lys Val Cys Ile Ala Gln Asp	
95	100 105
Ser Gln Thr Ala Val Cys Ile Ser His Arg Arg Leu Thr His Arg	
110	115 120
Met Lys Glu Ala Gly Val Asp His Arg Gln Trp Arg Gly Pro Ile	
125	130 135
Leu Ser Thr Cys Lys Gln Cys Pro Val Val Tyr Pro Ser Pro Val	
140	145 150
Cys Gly Ser Asp Gly His Thr Tyr Ser Phe Gln Cys Lys Leu Glu	
155	160 165
Tyr Gln Ala Cys Val Leu Gly Lys Gln Ile Ser Val Lys Cys Glu	
170	175 180
Gly His Cys Pro Cys Pro Ser Asp Lys Pro Thr Ser Thr Ser Arg	
185	190 195
Asn Val Lys Arg Ala Cys Ser Asp Leu Glu Phe Arg Glu Val Ala	
200	205 210
Asn Arg Leu Arg Asp Trp Phe Lys Ala Leu His Glu Ser Gly Ser	
215	220 225
Gln Asn Lys Lys Thr Lys Thr Leu Leu Arg Pro Glu Arg Ser Arg	
230	235 240
Phe Asp Thr Ser Ile Leu Pro Ile Cys Lys Asp Ser Leu Gly Trp	
245	250 255
Met Phe Asn Arg Leu Asp Thr Asn Tyr Asp Leu Leu Leu Asp Gln	
260	265 270
Ser Glu Leu Arg Ser Ile Tyr Leu Asp Lys Asn Glu Gln Cys Thr	
275	280 285
Lys Ala Phe Phe Asn Ser Cys Asp Thr Tyr Lys Asp Ser Leu Ile	
290	295 300
Ser Asn Asn Glu Trp Cys Tyr Cys Phe Gln Arg Gln Gln Asp Pro	
305	310 315
Pro Cys Gln Thr Glu Leu Ser Asn Ile Gln Lys Arg Gln Gly Val	
320	325 330
Lys Lys Leu Leu Gly Gln Tyr Ile Pro Leu Cys Asp Glu Asp Gly	
335	340 345

Tyr Tyr Lys Pro Thr Gln Cys His Gly Ser Val Gly Gln Cys Trp  
 350 355 360  
 Cys Val Asp Arg Tyr Gly Asn Glu Val Met Gly Ser Arg Ile Asn  
 365 370 375  
 Gly Val Ala Asp Cys Ala Ile Asp Phe Glu Ile Ser Gly Asp Phe  
 380 385 390  
 Ala Ser Gly Asp Phe His Glu Trp Thr Asp Asp Glu Asp Asp Glu  
 395 400 405  
 Asp Asp Ile Met Asn Asp Glu Asp Glu Ile Glu Asp Asp Asp Glu  
 410 415 420  
 Asp Glu Gly Asp Asp Asp Asp Gly Gly Asp Asp His Asp Val Tyr  
 425 430 435

Ile

<210> 443  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic oligonucleotide probe  
 <400> 443  
 cagcaatatt cagaagcggc aaggg 25  
 <210> 444  
 <211> 28  
 <212> DNA  
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 <223> Synthetic oligonucleotide probe  
 <400> 444  
 catcatggtc atcaccacca tcatcatc 28  
 <210> 445  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic oligonucleotide probe  
 <400> 445  
 ggttactaca agccaacaca atgtcatggc agtgttggac agtgctgg 48  
 <210> 446  
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 <212> DNA  
 <213> Homo sapiens

<400> 446

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cagggatggg cgacaagatc tggtgcctt tccccgtgt cttctggcc 150  
gctctgcctc cgggtgctgt gcttggggcg gccggcttca caccttcct 200  
cgatagcgac ttcaccttta cccttccgc cggccagaag gagtgttct 250  
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TOP SECRET - H302 FOOT

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<211> 229

<212> PRT

<213> Homo sapiens

<400> 447

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 20 25 30

Ser Leu Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys  
 35 40 45

Glu Cys Phe Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile  
 50 55 60

Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His  
 65 70 75

Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe Glu Gln Arg Lys  
 80 85 90

Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly Asp Tyr Met  
 95 100 105

Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys Val Ile

110 115 120  
 Phe Phe Glu Leu Ile Leu Asp Asn Met Gly Glu Gln Ala Gln Glu  
 125 130 135  
 Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp  
 140 145 150  
 Met Lys Leu Glu Asp Ile Leu Glu Ser Ile Asn Ser Ile Lys Ser  
 155 160 165  
 Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu Leu Arg Ala Phe  
 170 175 180  
 Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp Arg Val  
 185 190 195  
 Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val Val Ser  
 200 205 210  
 Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys Arg  
 215 220 225

Lys Ser Arg Thr

<210> 448  
 <211> 23  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

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<210> 449  
 <211> 23  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 449  
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<210> 450  
 <211> 43  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

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<210> 451  
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 <212> DNA  
 <213> Homo sapiens

<400> 451  
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 aaaaaaaaa 859

<210> 452  
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 <212> PRT  
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 20 25 30  
 Lys Glu Leu Pro Ser Pro Arg Ile Ser Cys Pro Lys Gly Ser Lys  
 35 40 45  
 Ala Tyr Gly Ser Pro Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser



50	55	60
Trp Met Asp Ala Asp Leu Ala Cys Gln Lys Arg Pro Ser Gly Lys		
65	70	75
Leu Val Ser Val Leu Ser Gly Ala Glu Gly Ser Phe Val Ser Ser		
80	85	90
Leu Val Arg Ser Ile Ser Asn Ser Tyr Ser Tyr Ile Trp Ile Gly		
95	100	105
Leu His Asp Pro Thr Gln Gly Ser Glu Pro Asp Gly Asp Gly Trp		
110	115	120
Glu Trp Ser Ser Thr Asp Val Met Asn Tyr Phe Ala Trp Glu Lys		
125	130	135
Asn Pro Ser Thr Ile Leu Asn Pro Gly His Cys Gly Ser Leu Ser		
140	145	150
Arg Ser Thr Gly Phe Leu Lys Trp Lys Asp Tyr Asn Cys Asp Ala		
155	160	165
Lys Leu Pro Tyr Val Cys Lys Phe Lys Asp		
170	175	

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 <212> DNA  
 <213> Homo sapiens

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<400> 454

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Pro Thr Gly Val Ser Asp Cys Val Thr Ile Ala Thr Cys Thr Thr  
35 40 45

Asn Glu Thr Met Cys Lys Thr Thr Leu Tyr Ser Arg Glu Ile Val  
50 55 60

Tyr Pro Phe Gln Gly Asp Ser Thr Val Thr Lys Ser Cys Ala Ser  
65 70 75

Lys Cys Lys Pro Ser Asp Val Asp Gly Ile Gly Gln Thr Leu Pro  
80 85 90

Val Ser Cys Cys Asn Thr Glu Leu Cys Asn Val Asp Gly Ala Pro  
95 100 105

Ala Leu Asn Ser Leu His Cys Gly Ala Leu Thr Leu Leu Pro Leu  
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Leu Ser Leu Arg Leu  
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<212> DNA

<213> Homo sapiens

<400> 455

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ggcggccacc ctctgctggg agtgagcgcc acctgaact cggttctcaa 250

ttccaacgct atcaagaacc tgccccacc gctgggcggc gctgcggggc 300

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aataagtacc agaccattga caactaccag ccgtaccggt gcgcagagga 400

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 catttaaaaa aaaaaaaa 1518

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 <211> 266  
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 35 40 45  
 Pro Pro Pro Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val  
 50 55 60  
 Ser Ala Ala Pro Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln  
 65 70 75



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<210> 458  
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 <213> Homo sapiens

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N  
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 <211> 747  
 <212> PRT  
 <213> Homo sapiens

<400> 459

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Gly	Thr	Asp	Gln	Asp	Phe	Tyr	Ser	Leu	Leu	Gly	Val	Ser	Lys	Thr
			35						40				45	
Ala	Ser	Ser	Arg	Glu	Ile	Arg	Gln	Ala	Phe	Lys	Lys	Leu	Ala	Leu
			50						55				60	
Lys	Leu	His	Pro	Asp	Lys	Asn	Pro	Asn	Asn	Pro	Asn	Ala	His	Gly
			65						70				75	
Asp	Phe	Leu	Lys	Ile	Asn	Arg	Ala	Tyr	Glu	Val	Leu	Lys	Asp	Glu
			80						85				90	
Asp	Leu	Arg	Lys	Lys	Tyr	Asp	Lys	Tyr	Gly	Glu	Lys	Gly	Leu	Glu
			95						100				105	
Asp	Asn	Gln	Gly	Gly	Gln	Tyr	Glu	Ser	Trp	Asn	Tyr	Tyr	Arg	Tyr
			110						115				120	
Asp	Phe	Gly	Ile	Tyr	Asp	Asp	Asp	Pro	Glu	Ile	Ile	Thr	Leu	Glu
			125						130				135	
Arg	Arg	Glu	Phe	Asp	Ala	Ala	Val	Asn	Ser	Gly	Glu	Leu	Trp	Phe
			140						145				150	
Val	Asn	Phe	Tyr	Ser	Pro	Gly	Cys	Ser	His	Cys	His	Asp	Leu	Ala
			155						160				165	
Pro	Thr	Trp	Arg	Asp	Phe	Ala	Lys	Glu	Val	Asp	Gly	Leu	Leu	Arg
			170						175				180	
Ile	Gly	Ala	Val	Asn	Cys	Gly	Asp	Asp	Arg	Met	Leu	Cys	Arg	Met
			185						190				195	
Lys	Gly	Val	Asn	Ser	Tyr	Pro	Ser	Leu	Phe	Ile	Phe	Arg	Ser	Gly



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Met Ala Pro Val Lys Tyr His Gly Asp	Arg Ser Lys Glu Ser Leu	
215	220	225
Val Ser Phe Ala Met Gln His Val Arg	Ser Thr Val Thr Glu Leu	
230	235	240
Trp Thr Gly Asn Phe Val Asn Ser Ile	Gln Thr Ala Phe Ala Ala	
245	250	255
Gly Ile Gly Trp Leu Ile Thr Phe Cys	Ser Lys Gly Gly Asp Cys	
260	265	270
Leu Thr Ser Gln Thr Arg Leu Arg Leu	Ser Gly Met Leu Phe Leu	
275	280	285
Asn Ser Leu Asp Ala Lys Glu Ile Tyr	Leu Glu Val Ile His Asn	
290	295	300
Leu Pro Asp Phe Glu Leu Leu Ser Ala	Asn Thr Leu Glu Asp Arg	
305	310	315
Leu Ala His His Arg Trp Leu Leu Phe	Phe His Phe Gly Lys Asn	
320	325	330
Glu Asn Ser Asn Asp Pro Glu Leu Lys	Lys Leu Lys Thr Leu Leu	
335	340	345
Lys Asn Asp His Ile Gln Val Gly Arg	Phe Asp Cys Ser Ser Ala	
350	355	360
Pro Asp Ile Cys Ser Asn Leu Tyr Val	Phe Gln Pro Ser Leu Ala	
365	370	375
Val Phe Lys Gly Gln Gly Thr Lys Glu	Tyr Glu Ile His His Gly	
380	385	390
Lys Lys Ile Leu Tyr Asp Ile Leu Ala	Phe Ala Lys Glu Ser Val	
395	400	405
Asn Ser His Val Thr Thr Leu Gly Pro	Gln Asn Phe Pro Ala Asn	
410	415	420
Asp Lys Glu Pro Trp Leu Val Asp Phe	Phe Ala Pro Trp Cys Pro	
425	430	435
Pro Cys Arg Ala Leu Leu Pro Glu Leu	Arg Arg Ala Ser Asn Leu	
440	445	450
Leu Tyr Gly Gln Leu Lys Phe Gly Thr	Leu Asp Cys Thr Val His	
455	460	465
Glu Gly Leu Cys Asn Met Tyr Asn Ile	Gln Ala Tyr Pro Thr Thr	
470	475	480
Val Val Phe Asn Gln Ser Asn Ile His	Glu Tyr Glu Gly His His	
485	490	495



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<210> 462  
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<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 462  
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<210> 463  
<211> 1818  
<212> DNA  
<213> Homo sapiens

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 <211> 300  
 <212> PRT  
 <213> Homo sapiens

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130200T 130200T

Arg Lys Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly  
35 40 45

His Gly Ile Gly Arg Gln Thr Thr Tyr Glu Phe Ala Lys Arg Gln  
50 55 60

Ser Ile Leu Val Leu Trp Asp Ile Asn Lys Arg Gly Val Glu Glu  
65 70 75

Thr Ala Ala Glu Cys Arg Lys Leu Gly Val Thr Ala His Ala Tyr  
80 85 90

Val Val Asp Cys Ser Asn Arg Glu Glu Ile Tyr Arg Ser Leu Asn  
95 100 105

Gln Val Lys Lys Glu Val Gly Asp Val Thr Ile Val Val Asn Asn  
110 115 120

Ala Gly Thr Val Tyr Pro Ala Asp Leu Leu Ser Thr Lys Asp Glu  
125 130 135

Glu Ile Thr Lys Thr Phe Glu Val Asn Ile Leu Gly His Phe Trp  
140 145 150

Ile Thr Lys Ala Leu Leu Pro Ser Met Met Glu Arg Asn His Gly  
155 160 165

His Ile Val Thr Val Ala Ser Val Cys Gly His Glu Gly Ile Pro  
170 175 180

Tyr Leu Ile Pro Tyr Cys Ser Ser Lys Phe Ala Ala Val Gly Phe  
185 190 195

His Arg Gly Leu Thr Ser Glu Leu Gln Ala Leu Gly Lys Thr Gly  
200 205 210

Ile Lys Thr Ser Cys Leu Cys Pro Val Phe Val Asn Thr Gly Phe  
215 220 225

Thr Lys Asn Pro Ser Thr Arg Leu Trp Pro Val Leu Glu Thr Asp  
230 235 240

Glu Val Val Arg Ser Leu Ile Asp Gly Ile Leu Thr Asn Lys Lys  
245 250 255

Met Ile Phe Val Pro Ser Tyr Ile Asn Ile Phe Leu Arg Leu Gln  
260 265 270

Lys Phe Leu Pro Glu Arg Ala Ser Ala Ile Leu Asn Arg Met Gln  
275 280 285

Asn Ile Gln Phe Glu Ala Val Val Gly His Lys Ile Lys Met Lys  
290 295 300

<210> 465  
<211> 1547  
<212> DNA  
<213> Homo sapiens

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 gcgcgacgcc cggcgagcc cagaccaggg ccggcagcag gcggagcgga 500  
 ggagcgtgct gcggggcttc tgcgccaact ccagcctggc cttccccacc 550  
 aaggagcgcg cattcgacga catccccaac tcggagctga gccacctgat 600  
 cgtggacgac cggcacgggg ccatctactg ctacgtgccc aagggtggcct 650  
 gcaccaactg gaagcgcgtg atgatcgtgc tgagcggaag cctgctgcac 700  
 cgcggtgcmc cctaccgca cccgctgcmc atcccgcmc agcacgtgca 750  
 caacgccagc gcgcacctga ccttcaaaa gttctggcmc cgctacggga 800  
 agctctcccc ccacctcatg aaggtcaagc tcaagaagta caccaagttc 850  
 ctcttcgtgc gcgaccctt cgtgcgcctg atctccgct tccgagcaa 900  
 gttcgagctg gagaacgagg agttctaccg caagttcgcc gtgcccacgc 950  
 tgcggtgta cgccaaccac accagcctgc ccgcctcggc gcgcgaggcc 1000  
 ttccgcgtg gcctcaaggt gtccttcgcc aacttcatcc agtacctgct 1050  
 ggaccgcac acggagaagc tggcgccctt caacgagcac tggcggcagg 1100  
 tgtaccgcct ctgccaccgc tgccagatcg actacgactt cgtggggaag 1150  
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 ggaccggcag ctccgcttcc ccccgagcta ccggaacagg accgccagca 1250  
 gctgggagga ggactgggtc gccaaagatcc ccctggcctg gaggcagcag 1300  
 ctgtataaac tctacgaggc cgactttggt ctcttcggct accccaagcc 1350  
 cgaaaacctc ctccgagact gaaagcttcc gcgttgcttt ttctcgcgtg 1400  
 cctggaacct gacgcacgcg cactccagtt tttttatgac ctacgatttt 1450

atcgatattg tttttaaga ttaatatatt tcaggtattt aatacga 1547

<210> 466

<211> 414

<212> PRT

<213> Homo sapiens

<400> 466

Met Thr Lys Ala Arg Leu Phe Arg Leu Trp Leu Val Leu Gly Ser  
1 5 10 15

Val Phe Met Ile Leu Leu Ile Ile Val Tyr Trp Asp Ser Ala Gly  
20 25 30

Ala Ala His Phe Tyr Leu His Thr Ser Phe Ser Arg Pro His Thr  
35 40 45

Gly Pro Pro Leu Pro Thr Pro Gly Pro Asp Arg Asp Arg Glu Leu  
50 55 60

Thr Ala Asp Ser Asp Val Asp Glu Phe Leu Asp Lys Phe Leu Ser  
65 70 75

Ala Gly Val Lys Gln Ser Asp Leu Pro Arg Lys Glu Thr Glu Gln  
80 85 90

Pro Pro Ala Pro Gly Ser Met Glu Glu Ser Val Arg Gly Tyr Asp  
95 100 105

Trp Ser Pro Arg Asp Ala Arg Arg Ser Pro Asp Gln Gly Arg Gln  
110 115 120

Gln Ala Glu Arg Arg Ser Val Leu Arg Gly Phe Cys Ala Asn Ser  
125 130 135

Ser Leu Ala Phe Pro Thr Lys Glu Arg Ala Phe Asp Asp Ile Pro  
140 145 150

Asn Ser Glu Leu Ser His Leu Ile Val Asp Asp Arg His Gly Ala  
155 160 165

Ile Tyr Cys Tyr Val Pro Lys Val Ala Cys Thr Asn Trp Lys Arg  
 170 175 180

Val Met Ile Val Leu Ser Gly Ser Leu Leu His Arg Gly Ala Pro  
185 190 195

Tyr Arg Asp Pro Leu Arg Ile Pro Arg Glu His Val His Asn Ala  
200 205 210

Ser Ala His Leu Thr Phe Asn Lys Phe Trp Arg Arg Tyr Gly Lys  
215 220 225

Leu Ser Arg His Leu Met Lys Val Lys Leu Lys Lys Tyr Thr Lys  
230 235 240

Phe Leu Phe Val Arg Asp Pro Phe Val Arg Leu Ile Ser Ala Phe  
 245 250 255  
 Arg Ser Lys Phe Glu Leu Glu Asn Glu Glu Phe Tyr Arg Lys Phe  
 260 265 270  
 Ala Val Pro Met Leu Arg Leu Tyr Ala Asn His Thr Ser Leu Pro  
 275 280 285  
 Ala Ser Ala Arg Glu Ala Phe Arg Ala Gly Leu Lys Val Ser Phe  
 290 295 300  
 Ala Asn Phe Ile Gln Tyr Leu Leu Asp Pro His Thr Glu Lys Leu  
 305 310 315  
 Ala Pro Phe Asn Glu His Trp Arg Gln Val Tyr Arg Leu Cys His  
 320 325 330  
 Pro Cys Gln Ile Asp Tyr Asp Phe Val Gly Lys Leu Glu Thr Leu  
 335 340 345  
 Asp Glu Asp Ala Ala Gln Leu Leu Gln Leu Leu Gln Val Asp Arg  
 350 355 360  
 Gln Leu Arg Phe Pro Pro Ser Tyr Arg Asn Arg Thr Ala Ser Ser  
 365 370 375  
 Trp Glu Glu Asp Trp Phe Ala Lys Ile Pro Leu Ala Trp Arg Gln  
 380 385 390  
 Gln Leu Tyr Lys Leu Tyr Glu Ala Asp Phe Val Leu Phe Gly Tyr  
 395 400 405  
 Pro Lys Pro Glu Asn Leu Leu Arg Asp  
 410

<210> 467  
 <211> 1071  
 <212> DNA  
 <213> Homo sapiens

<400> 467  
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 ctttgaggt gaaagaggcc cagagtagag agagagagag accgacgtac 100  
 acgggatggc tacgggaacg cgctatgccg ggaaggtggt ggtcgtgacc 150  
 gggggcgggc gcggcatcgg agctgggacg gtgcgcgcct tcgtgaacag 200  
 cggggcccga gtggttatct gcgacaagga tgagtctggg ggccggggccc 250  
 tggagcagga gctccctgga gctgtcttta tcctctgtga tgtgactcag 300  
 gaagatgatg tgaagaccct ggtttctgag accatccgcc gatttggccg 350  
 cctggattgt gttgtcaaca acgctggcca ccacccaccc ccacagaggc 400



total=1304700

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 tcaagggaaat gtcataca tctccagcct ggtgggggca atcggccagg 550  
 cccaggcagt tccctatgtg gccaccaagg gggcagtaac agccatgacc 600  
 aaagcttttg ccttgatga aagtccatat ggtgtccgag tcaactgtat 650  
 ctccccagga aacatctgga ccccgctgtg ggaggagctg gcagccttaa 700  
 tgccagaccc tagggccaca atccgagagg gcatgctggc ccagccactg 750  
 ggccgcatgg gccagcccgc tgaggtcggg gctgcggcag tgttctgtgc 800  
 ctccgaagcc aacttctgca cgggcattga actgctcgtg acgggggggtg 850  
 cagagctggg gtacgggtgc aaggccagtc ggagcaccac cgtggacgcc 900  
 cccgatatcc ctctctgatt tctctcattt ctacttgggg ccccttcct 950  
 aggactctcc caccocaaac tccaacctgt atcagatgca gcccocaaagc 1000  
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 ccataaaaac gatttgcagc c 1071

<210> 468  
 <211> 270  
 <212> PRT  
 <213> Homo sapiens

<400> 468  
 Met Ala Thr Gly Thr Arg Tyr Ala Gly Lys Val Val Val Val Thr  
 1 5 10 15  
 Gly Gly Gly Arg Gly Ile Gly Ala Gly Ile Val Arg Ala Phe Val  
 20 25 30  
 Asn Ser Gly Ala Arg Val Val Ile Cys Asp Lys Asp Glu Ser Gly  
 35 40 45  
 Gly Arg Ala Leu Glu Gln Glu Leu Pro Gly Ala Val Phe Ile Leu  
 50 55 60  
 Cys Asp Val Thr Gln Glu Asp Asp Val Lys Thr Leu Val Ser Glu  
 65 70 75  
 Thr Ile Arg Arg Phe Gly Arg Leu Asp Cys Val Val Asn Asn Ala  
 80 85 90  
 Gly His His Pro Pro Pro Gln Arg Pro Glu Glu Thr Ser Ala Gln  
 95 100 105  
 Gly Phe Arg Gln Leu Leu Glu Leu Asn Leu Leu Gly Thr Tyr Thr  
 110 115 120

Leu Thr Lys Leu Ala Leu Pro Tyr Leu Arg Lys Ser Gln Gly Asn  
 125 130 135  
 Val Ile Asn Ile Ser Ser Leu Val Gly Ala Ile Gly Gln Ala Gln  
 140 145 150  
 Ala Val Pro Tyr Val Ala Thr Lys Gly Ala Val Thr Ala Met Thr  
 155 160 165  
 Lys Ala Leu Ala Leu Asp Glu Ser Pro Tyr Gly Val Arg Val Asn  
 170 175 180  
 Cys Ile Ser Pro Gly Asn Ile Trp Thr Pro Leu Trp Glu Glu Leu  
 185 190 195  
 Ala Ala Leu Met Pro Asp Pro Arg Ala Thr Ile Arg Glu Gly Met  
 200 205 210  
 Leu Ala Gln Pro Leu Gly Arg Met Gly Gln Pro Ala Glu Val Gly  
 215 220 225  
 Ala Ala Ala Val Phe Leu Ala Ser Glu Ala Asn Phe Cys Thr Gly  
 230 235 240  
 Ile Glu Leu Leu Val Thr Gly Gly Ala Glu Leu Gly Tyr Gly Cys  
 245 250 255  
 Lys Ala Ser Arg Ser Thr Pro Val Asp Ala Pro Asp Ile Pro Ser  
 260 265 270

<210> 469  
 <211> 687  
 <212> DNA  
 <213> Homo sapiens

<400> 469  
 aggcgggcag cagctgcagg ctgacctgac agcttgccgg aatggactgg 50  
 cctcacaacc tgctgtttct tcttaccatt tccatcttcc tggggctggg 100  
 ccagcccagg agccccaaaa gcaagaggaa ggggcaagg cggcctgggc 150  
 ccctggcccc tggccctcac caggtgccac tggacctggt gtcacggatg 200  
 aaaccgtatg cccgcatgga ggagtatgag aggaacatcg aggagatggt 250  
 ggcccagctg aggaacagct cagagctggc ccagagaaag tgtgaggtca 300  
 acttgacgtg gtggatgtcc aacaagagga gcctgtctcc ctggggctac 350  
 agcatcaacc acgaccccag ccgtatcccc gtggacctgc cggaggcacg 400  
 gtgcctgtgt ctgggctgtg tgaacccctt caccatgcag gaggaccgca 450  
 gcatggtgag cgtgccgtg ttcagccagg ttcctgtgcg ccgccgcctc 500  
 tgcccggcac cgccccgcac agggccttgc cgccagcgcg cagtcattga 550

gaccatcgct gtgggctgca cctgcatctt ctgaatcacc tggcccagaa 600  
 gccaggccag cagcccagaga ccatactctt tgcacctttg tgccaagaaa 650  
 ggccatgaa aagtaaacac tgacttttga aagcaag 687

<210> 470  
 <211> 180  
 <212> PRT  
 <213> Homo sapiens

<400> 470  
 Met Asp Trp Pro His Asn Leu Leu Phe Leu Leu Thr Ile Ser Ile  
 1 5 10 15  
 Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys  
 20 25 30  
 Gly Gln Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val  
 35 40 45  
 Pro Leu Asp Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu  
 50 55 60  
 Glu Tyr Glu Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn  
 65 70 75  
 Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu  
 80 85 90  
 Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile  
 95 100 105  
 Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg  
 110 115 120  
 Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu Asp  
 125 130 135  
 Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val Arg  
 140 145 150  
 Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg Gln  
 155 160 165  
 Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe  
 170 175 180

<210> 471  
 <211> 2368  
 <212> DNA  
 <213> Homo sapiens

<400> 471  
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 aaacccggcg ggcgagcgag gctgcgggcc ggccgctgcc cttccccaca 100

ctccccgccg agaagcctcg ctggcgccc aacatggcgg gtggcgctg 150  
 cggcccgag ctaacggcgc tcctggccgc ctggatcgcg gctgtggcg 200  
 cgacggcagg ccccaggag gccgcgctgc cgccggagca gagccgggtc 250  
 cagcccatga ccgcctcaa ctggacgctg gtgatggagg gcgagtggat 300  
 gctgaaatct tacgccccat ggtgtccatc ctgccagcag actgattcag 350  
 aatgggaggc ttttgcaaag aatggtgaaa tacttcagat cagtgtgggg 400  
 aaggtagatg tcattcaaga accaggtttg agtggccgct tctttgtcac 450  
 cactctccca gcattttttc atgcaaagga tgggatattc cgccgttatt 500  
 gtggcccagg aatcttcgaa gacctgcaga attatatctt agagaagaaa 550  
 tggcaatcag tcgagcctct gactggctgg-aaatccccag cttctctaac 600  
 gatgtctgga atggctggc ttttagcat ctctggcaag atatggcatc 650  
 ttcacaacta tttcacagt actcttgaa ttctgttg gtgttcttat 700  
 gtgtttttcg tcatagccac cttggtttt gccctttta tgggtctggt 750  
 cttggtgta atatcagaat gtttctatgt gccacttcca aggcatctat 800  
 ctgagcgctt tgagcagaat cggagatcag aggaggctca tagagctgaa 850  
 cagttgcagg atcggaggga gaaaaagat gattcaaatg aagaagaaaa 900  
 caaagacagc cttgtagatg atgaagaaga gaaagaagat cttggcgatg 950  
 aggatgaagc agaggaagaa gaggaggagg acaacttggc tgctggtgtg 1000  
 gatgaggaga gaagtgggc caatgatcag gggccccag gagaggacgg 1050  
 tgtgacccgg gaggaagtag agcctgagga ggctgaagaa ggcattctctg 1100  
 agcaaccctg cccagctgac acagaggtgg tgaagactc cttgaggcag 1150  
 cgtaaaagtc agcatgctga caagggactg tagatttaat gatgcgtttt 1200  
 caagaataca caccaaaaca atatgtcagc ttccctttgg cctgcagttt 1250  
 gtaccaaata ctttaatttt cctgaatgag caagcttctc ttaaaagatg 1300  
 ctctctagtc atttggtctc atggcagtaa gcctcatgta tactaaggag 1350  
 agtcttccag gtgtgacaat caggatatag aaaaacaaac gtagtggttg 1400  
 gatctgtttg gagactggga tgggaacaag ttcatttact taggggtcag 1450  
 agagtctcga ccagaggagg ccattcccag tcctaatacag caccttccag 1500  
 agacaaggct gcaggccctg tgaaatgaaa gccaaagcag agccttggct 1550

cctgagcatc cccaaagtgt aacgtagaag ccttgcatcc ttttcttggtg 1600  
 taaagtattt atttttgtca aattgcagga aacatcaggc accacagtgc 1650  
 atgaaaaatc tttcacagct agaaattgaa agggccttgg gtatagagag 1700  
 cagctcagaa gtcatcccag ccctctgaat ctctgtgtct atgttttatt 1750  
 tcttaccttt aatttttcca gcatttccac catgggcatt caggtctctcc 1800  
 acactcttca ctattatctc ttggtcagag gactccaata acagccaggt 1850  
 ttacatgaac tgtgtttggt cattctgacc taaggggttt agataatcag 1900  
 taaccataac ccctgaagct gtgactgcc aacatctcaa atgaaatggt 1950  
 gtggccatca gagactcaaa aggaagtaag gattttacaa gacagattaa 2000  
 aaaaaaattg-ttttgtccaa-aatatagttg ttgttgattt ttttttaagt 2050  
 tttctaagca atatttttca agccagaagt cctctaagtc ttgccagtac 2100  
 aaggtagtct tgtgaagaaa agttgaatac tgttttgttt tcatctcaag 2150  
 gggttccctg ggtcttgaac tactttaata ataactaaaa aaccacttct 2200  
 gattttcctt cagtgatgtg cttttggtga aagaattaat gaactccagt 2250  
 acctgaaagt gaaagatttg attttgtttc catcttctgt aatcttccaa 2300  
 agaattatat ctttgtaaat ctctcaatac tcaatctact gtaagtaccc 2350  
 agggaggcta atttcttt 2368

<210> 472  
 <211> 349  
 <212> PRT  
 <213> Homo sapiens

<400> 472  
 Met Ala Gly Gly Arg Cys Gly Pro Gln Leu Thr Ala Leu Leu Ala  
 1 5 10 15  
 Ala Trp Ile Ala Ala Val Ala Ala Thr Ala Gly Pro Glu Glu Ala  
 20 25 30  
 Ala Leu Pro Pro Glu Gln Ser Arg Val Gln Pro Met Thr Ala Ser  
 35 40 45  
 Asn Trp Thr Leu Val Met Glu Gly Glu Trp Met Leu Lys Phe Tyr  
 50 55 60  
 Ala Pro Trp Cys Pro Ser Cys Gln Gln Thr Asp Ser Glu Trp Glu  
 65 70 75  
 Ala Phe Ala Lys Asn Gly Glu Ile Leu Gln Ile Ser Val Gly Lys  
 80 85 90

Val Asp Val Ile Gln Glu Pro Gly Leu Ser Gly Arg Phe Phe Val  
 95 100 105  
 Thr Thr Leu Pro Ala Phe Phe His Ala Lys Asp Gly Ile Phe Arg  
 110 115 120  
 Arg Tyr Arg Gly Pro Gly Ile Phe Glu Asp Leu Gln Asn Tyr Ile  
 125 130 135  
 Leu Glu Lys Lys Trp Gln Ser Val Glu Pro Leu Thr Gly Trp Lys  
 140 145 150  
 Ser Pro Ala Ser Leu Thr Met Ser Gly Met Ala Gly Leu Phe Ser  
 155 160 165  
 Ile Ser Gly Lys Ile Trp His Leu His Asn Tyr Phe Thr Val Thr  
 170 175 180  
 Leu Gly Ile Pro Ala Trp Cys Ser Tyr Val Phe Phe Val Ile Ala  
 185 190 195  
 Thr Leu Val Phe Gly Leu Phe Met Gly Leu Val Leu Val Val Ile  
 200 205 210  
 Ser Glu Cys Phe Tyr Val Pro Leu Pro Arg His Leu Ser Glu Arg  
 215 220 225  
 Ser Glu Gln Asn Arg Arg Ser Glu Glu Ala His Arg Ala Glu Gln  
 230 235 240  
 Leu Gln Asp Ala Glu Glu Glu Lys Asp Asp Ser Asn Glu Glu Glu  
 245 250 255  
 Asn Lys Asp Ser Leu Val Asp Asp Glu Glu Glu Lys Glu Asp Leu  
 260 265 270  
 Gly Asp Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Asp Asn Leu  
 275 280 285  
 Ala Ala Gly Val Asp Glu Glu Arg Ser Glu Ala Asn Asp Gln Gly  
 290 295 300  
 Pro Pro Gly Glu Asp Gly Val Thr Arg Glu Glu Val Glu Pro Glu  
 305 310 315  
 Glu Ala Glu Glu Gly Ile Ser Glu Gln Pro Cys Pro Ala Asp Thr  
 320 325 330  
 Glu Val Val Glu Asp Ser Leu Arg Gln Arg Lys Ser Gln His Ala  
 335 340 345  
 Asp Lys Gly Leu

<210> 473

<211> 24

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 473  
gtccagccca tgaccgcctc caac 24

<210> 474  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 474  
ctctcctcat ccacaccagc agcc 24

<210> 475  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 475  
gtggatgctg aaattttacg ccccatgggtg tccatcctgc cagc 44

<210> 476  
<211> 2478  
<212> DNA  
<213> Homo sapiens

<400> 476  
atctggttga actacttaag ctttaatttgt taaactccgg taagtaccta 50  
gcccacatga ttgactcag agattctctt ttgtccacag acagtcattc 100  
caggggcaga aagaaaagag ctcccaaag ctatatctat tcaggggctc 150  
tcaagaacaa tggaaatca tctgattta gaaaatttgg atgaagatgg 200  
atatactcaa ttacacttcg actctcaaag caataccagg atagctgttg 250  
tttcagagaa aggatcgtgt gctgcatctc ctccttggcg cctcattgct 300  
gtaatttttg gaatcctatg cttggttaata ctgggtgatg ctgtggctcct 350  
gggtaccatg ggggttcttt ccagcccttg tcctcctaat tggattatat 400  
atgagaagag ctgttatcta ttcagcatgt cactaaattc ctgggatgga 450  
agtaaaagac aatgctggca actgggctct aatctcctaa agatagacag 500  
ctcaaataga ttgggattta tagtaaaaca agtgtcttcc caacctgata 550  
attcattttg gataggcctt tctcgcccc agactgaggt accatggctc 600

tgggaggatg gatcaacatt ctcttctaac ttatttcaga tcagaaccac 650  
 agctacccaa gaaaacccat ctccaaatig tgtatggatt cacgtgtcag 700  
 tcatttatga ccaactgtgt agtgtgccct catatagtat ttgtgagaag 750  
 aagttttcaa tgtaagagga aggggtggaga aggagagaga aatatgtgag 800  
 gtagtaagga ggacagaaaa cagaacagaa aagagtaaca gctgagggtca 850  
 agataaatgc agaaaatggt tagagagctt ggccaactgt aatcttaacc 900  
 aagaaattga agggagaggc tgtgatttct gtatttgtcg acctacaggt 950  
 aggctagtat tttttttcta gttagtagat ccctagacat ggaatcaggg 1000  
 cagccaagct tgagttttta ttttttattt atttttttt ttgagatagg 1050  
 gtctcacttt gttaccagg ctggagtga gtggcacaat ctgcactcac 1100  
 tgcagctatc tctcgectca gccctcaag tagctgggac tacagggtga 1150  
 tgccaccatg ccaggctaatt ttttggtgtt tttttagag actgggtttt 1200  
 gccatgttga ccaagctggt ctctaactcc tgggcttaag tgatctgcc 1250  
 gccttggcct cccaaagtgc tgggattaca gatgtgagcc accacacctg 1300  
 gcccgaagct tgaattttca ttctgccatt gacttggcat ttaccttggg 1350  
 taagccataa gcgaatctta atttctggct ctatcagagt tgtttcatgc 1400  
 tcaacaatgc cattgaagtg cacggtgtgt tgccacgatt tgacctcaa 1450  
 cttctagcag tatatcagtt atgaactgag ggtgaaatat atttctgaat 1500  
 agctaaatga agaaatggga aaaaatcttc accacagtca gagcaatttt 1550  
 attattttca tcagtatgat cataattatg attatcatct tagtaaaaag 1600  
 caggaactcc tactttttct ttatcaatta aatagctcag agagtacatc 1650  
 tgccatatct ctaatagaat cttttttttt ttttttttt tttgagacag 1700  
 agtttcgctc ttgttgccca ggctggagtg caacggcacg atctcggctc 1750  
 accgcaacct ccgccccctg ggttcaagca attctcctgc ctcagcctcc 1800  
 caagtagctg ggattacagt caggcaccac cacaccggc taattttgta 1850  
 tttttttagt agagacaggg tttctccatg tcggtcaggg tagtcccgaa 1900  
 ctctgacct caagtgatct gcctgcctcg gcctcccaag tgctgggatt 1950  
 acaggcgtga gccactgcac ccagcctaga atcttgtata atatgtaatt 2000  
 gtagggaaac tgctctcata ggaaagtttt ctgcttttta aatacaaaaa 2050



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 tcattggaac aagtattaac attttgaat atgttttatt agttttgtga 2150  
 tgtactgttt tacaattttt accatttttt tcagtaatta ctgtaaaatg 2200  
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 ttttcatact ttcccaactgg tgctattttt atttccaatg gatattttctg 2300  
 tattactagg gaggcattta cagtcctcta atgttgatta atatgtgaaa 2350  
 agaaattgta ccaattttac taaattatgc agttttaaag ggatgatttt 2400  
 atgttatgtg gatttcattt caataaaaaa aaactcttat caaaaaaaaaa 2450  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2478

<210> 477  
 <211> 201  
 <212> PRT  
 <213> Homo sapiens

<400> 477  
 Met Glu Tyr His Pro Asp Leu Glu Asn Leu Asp Glu Asp Gly Tyr  
 1 5 10 15  
 Thr Gln Leu His Phe Asp Ser Gln Ser Asn Thr Arg Ile Ala Val  
 20 25 30  
 Val Ser Glu Lys Gly Ser Cys Ala Ala Ser Pro Pro Trp Arg Leu  
 35 40 45  
 Ile Ala Val Ile Leu Gly Ile Leu Cys Leu Val Ile Leu Val Ile  
 50 55 60  
 Ala Val Val Leu Gly Thr Met Gly Val Leu Ser Ser Pro Cys Pro  
 65 70 75  
 Pro Asn Trp Ile Ile Tyr Glu Lys Ser Cys Tyr Leu Phe Ser Met  
 80 85 90  
 Ser Leu Asn Ser Trp Asp Gly Ser Lys Arg Gln Cys Trp Gln Leu  
 95 100 105  
 Gly Ser Asn Leu Leu Lys Ile Asp Ser Ser Asn Glu Leu Gly Phe  
 110 115 120  
 Ile Val Lys Gln Val Ser Ser Gln Pro Asp Asn Ser Phe Trp Ile  
 125 130 135  
 Gly Leu Ser Arg Pro Gln Thr Glu Val Pro Trp Leu Trp Glu Asp  
 140 145 150  
 Gly Ser Thr Phe Ser Ser Asn Leu Phe Gln Ile Arg Thr Thr Ala  
 155 160 165  
 Thr Gln Glu Asn Pro Ser Pro Asn Cys Val Trp Ile His Val Ser

170

175

180

Val Ile Tyr Asp Gln Leu Cys Ser Val Pro Ser Tyr Ser Ile Cys  
 185 190 195

Glu Lys Lys Phe Ser Met  
 200

<210> 478  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 478  
 gtccacagac agtcatctca ggagcag 27

<210> 479  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 479  
 acaagtgtct tcccaacctg 20

<210> 480  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 480  
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<210> 481  
 <211> 51  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

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t 51

<210> 482  
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 <212> DNA  
 <213> Homo sapiens



<400> 482

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Pro	Ala	Ser	Arg	Ser	Phe	Pro	Asp	Pro	Arg	Gly	Leu	Tyr	His	Phe		80	85	90
Cys	Leu	Tyr	Trp	Asn	Arg	His	Ala	Gly	Arg	Leu	His	Leu	Leu	Tyr		95	100	105
Gly	Lys	Arg	Asp	Phe	Leu	Leu	Ser	Asp	Lys	Ala	Ser	Ser	Leu	Leu		110	115	120
Cys	Phe	Gln	His	Gln	Glu	Glu	Ser	Leu	Ala	Gln	Gly	Pro	Pro	Leu		125	130	135
Leu	Ala	Thr	Ser	Val	Thr	Ser	Trp	Trp	Ser	Pro	Gln	Asn	Ile	Ser		140	145	150
Leu	Pro	Ser	Ala	Ala	Ser	Phe	Thr	Phe	Ser	Phe	His	Ser	Pro	Pro		155	160	165
His	Thr	Ala	Ala	His	Asn	Ala	Ser	Val	Asp	Met	Cys	Glu	Leu	Lys		170	175	180
Arg	Asp	Leu	Gln	Leu	Leu	Ser	Gln	Phe	Leu	Lys	His	Pro	Gln	Lys		185	190	195
Ala	Ser	Arg	Arg	Pro	Ser	Ala	Ala	Pro	Ala	Ser	Gln	Gln	Leu	Gln		200	205	210
Ser	Leu	Glu	Ser	Lys	Leu	Thr	Ser	Val	Arg	Phe	Met	Gly	Asp	Met		215	220	225
Val	Ser	Phe	Glu	Glu	Asp	Arg	Ile	Asn	Ala	Thr	Val	Trp	Lys	Leu		230	235	240
Gln	Pro	Thr	Ala	Gly	Leu	Gln	Asp	Leu	His	Ile	His	Ser	Arg	Gln		245	250	255
Glu	Glu	Glu	Gln	Ser	Glu	Ile	Met	Glu	Tyr	Ser	Val	Leu	Leu	Pro		260	265	270
Arg	Thr	Leu	Phe	Gln	Arg	Thr	Lys	Gly	Arg	Ser	Gly	Glu	Ala	Glu		275	280	285
Lys	Arg	Leu	Leu	Leu	Val	Asp	Phe	Ser	Ser	Gln	Ala	Leu	Phe	Gln		290	295	300
Asp	Lys	Asn	Ser	Ser	Gln	Val	Leu	Gly	Glu	Lys	Val	Leu	Gly	Ile		305	310	315
Val	Val	Gln	Asn	Thr	Lys	Val	Ala	Asn	Leu	Thr	Glu	Pro	Val	Val		320	325	330
Leu	Thr	Phe	Gln	His	Gln	Leu	Gln	Pro	Lys	Asn	Val	Thr	Leu	Gln		335	340	345
Cys	Val	Phe	Trp	Val	Glu	Asp	Pro	Thr	Leu	Ser	Ser	Pro	Gly	His		350	355	360
Trp	Ser	Ser	Ala	Gly	Cys	Glu	Thr	Val	Arg	Arg	Glu	Thr	Gln	Thr				

FOOT 1202 FOOT

365	370	375
Ser Cys Phe Cys Asn His Leu Thr Tyr	Phe Ala Val Leu Met Val	
380	385	390
Ser Ser Val Glu Val Asp Ala Val His	Lys His Tyr Leu Ser Leu	
395	400	405
Leu Ser Tyr Val Gly Cys Val Val Ser	Ala Leu Ala Cys Leu Val	
410	415	420
Thr Ile Ala Ala Tyr Leu Cys Ser Arg	Val Pro Leu Pro Cys Arg	
425	430	435
Arg Lys Pro Arg Asp Tyr Thr Ile Lys	Val His Met Asn Leu Leu	
440	445	450
Leu Ala Val Phe Leu Leu Asp Thr Ser	Phe Leu Leu Ser Glu Pro	
455	460	465
Val Ala Leu Thr Gly Ser Glu Ala Gly	Cys Arg Ala Ser Ala Ile	
470	475	480
Phe Leu His Phe Ser Leu Leu Thr Cys	Leu Ser Trp Met Gly Leu	
485	490	495
Glu Gly Tyr Asn Leu Tyr Arg Leu Val	Val Glu Val Phe Gly Thr	
500	505	510
Tyr Val Pro Gly Tyr Leu Leu Lys Leu	Ser Ala Met Gly Trp Gly	
515	520	525
Phe Pro Ile Phe Leu Val Thr Leu Val	Ala Leu Val Asp Val Asp	
530	535	540
Asn Tyr Gly Pro Ile Ile Leu Ala Val	His Arg Thr Pro Glu Gly	
545	550	555
Val Ile Tyr Pro Ser Met Cys Trp Ile	Arg Asp Ser Leu Val Ser	
560	565	570
Tyr Ile Thr Asn Leu Gly Leu Phe Ser	Leu Val Phe Leu Phe Asn	
575	580	585
Met Ala Met Leu Ala Thr Met Val Val	Gln Ile Leu Arg Leu Arg	
590	595	600
Pro His Thr Gln Lys Trp Ser His Val	Leu Thr Leu Leu Gly Leu	
605	610	615
Ser Leu Val Leu Gly Leu Pro Trp Ala	Leu Ile Phe Phe Ser Phe	
620	625	630
Ala Ser Gly Thr Phe Gln Leu Val Val	Leu Tyr Leu Phe Ser Ile	
635	640	645
Ile Thr Ser Phe Gln Gly Phe Leu Ile	Phe Ile Trp Tyr Trp Ser	
650	655	660

Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu Lys Ser Asn  
665 670 675

Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser  
680 685 690

Ser Arg Ile

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<211> 516  
<212> DNA  
<213> Homo sapiens

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<221> unsure  
<222> 68, 70, 84, 147  
<223> unknown base

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cggtagccct gacaggctct gaaggctggc tgccgagcca gtgcatctt 200  
cctgcacttc tctgctcac ctgcctttcc tggatgggccc tcgaggggta 250  
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<210> 485  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 485  
ggcattggag cagtgtggtg tg 22

<210> 486  
<211> 24  
<212> DNA  
<213> Artificial Sequence



<220>  
<223> Synthetic oligonucleotide probe

<400> 486  
tggaggccta gatgcggctg gacg 24

<210> 487  
<211> 2849  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 2715  
<223> unknown base

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aagagggctc taggaaaaag ttttgatgg gattatgtgg aaactaccct 150  
gcgattctct gctgccagag caggctcggc gcttccaccc cagtgcagcc 200  
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ccgccgtgag tgagctctca cccagtcag ccaaagtgc ctcttcgggc 300  
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cggagtacaa gatcctcagc atgagagaat tattactgtg tctactaatg 450  
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gtttgatgaa agatttgggc ttgaagacc agaagatgac atatgcaagt 600  
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<210> 488  
 <211> 345  
 <212> PRT  
 <213> Homo sapiens

<400> 488

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Gln	Phe	Ser	Ser	Asn	Lys	Glu	Gln	Asn	Gly	Val	Gln	Asp	Pro	Gln	35	40	45	
His	Glu	Arg	Ile	Ile	Thr	Val	Ser	Thr	Asn	Gly	Ser	Ile	His	Ser	50	55	60	
Pro	Arg	Phe	Pro	His	Thr	Tyr	Pro	Arg	Asn	Thr	Val	Leu	Val	Trp	65	70	75	
Arg	Leu	Val	Ala	Val	Glu	Glu	Asn	Val	Trp	Ile	Gln	Leu	Thr	Phe	80	85	90	
Asp	Glu	Arg	Phe	Gly	Leu	Glu	Asp	Pro	Glu	Asp	Asp	Ile	Cys	Lys	95	100	105	
Tyr	Asp	Phe	Val	Glu	Val	Glu	Glu	Pro	Ser	Asp	Gly	Thr	Ile	Leu	110	115	120	
Gly	Arg	Trp	Cys	Gly	Ser	Gly	Thr	Val	Pro	Gly	Lys	Gln	Ile	Ser	125	130	135	
Lys	Gly	Asn	Gln	Ile	Arg	Ile	Arg	Phe	Val	Ser	Asp	Glu	Tyr	Phe	140	145	150	
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Gln	Phe	Thr	Glu	Ala	Val	Ser	Pro	Ser	Val	Leu	Pro	Pro	Ser	Ala	170	175	180	
Leu	Pro	Leu	Asp	Leu	Leu	Asn	Asn	Ala	Ile	Thr	Ala	Phe	Ser	Thr	185	190	195	

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200 205 210

Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly Lys  
215 220 225

Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu  
230 235 240

Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe  
245 250 255

Ser Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe  
260 265 270

Trp Pro Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala  
275 280 285

Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys  
290 295 300

Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr  
305 310 315

Gly Val Arg Gly Leu His Lys Ser Leu Thr Asp Val Ala Leu Glu  
320 325 330

His His Glu Glu Cys Asp Cys Val Cys Arg Gly Ser Thr Gly Gly  
335 340 345

<210> 489

<211> 21

<212> DNA

<213> Artificial Sequence

$\langle 220 \rangle$

<223> Synthetic oligonucleotide probe

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<210> 490

<211> 40

<212> DNA

### <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 490

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<210> 491

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 492  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 492  
acaacaggca cagttccac 20

<210> 493  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 493  
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<210> 494  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 494  
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<210> 495  
<211> 3283  
<212> DNA  
<213> Homo sapiens

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ggacactgaa gagacaaatt cttatccttt ttaacataat cctaatttcc 150  
aaactccttg gggctagatg gtttccctaaa actctgccct gtgatgtcac 200  
tctggatgtt ccaaagaacc atgtgatcgt ggactgcaca gacaagcatt 250  
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ccatctggta gagatcgatt tcagatgcaa ctgtgtacct attccactgg 400  
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 aatctgtcag gaaatctcat tagccaaact cttaatggca gtgaattcca 1700  
 accttagca gagctgagat atttggaact ctccaacaac cggttgatt 1750  
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<210> 496

<211> 1049

<212> PRT

<213> Homo sapiens

<400> 496

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20 25 30

Pro Lys Thr Leu Pro Cys Asp Val Thr Leu Asp Val Pro Lys Asn  
35 40 45

His Val Ile Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro  
50 55 60

Gly Gly Ile Pro Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn  
65 70 75

His Ile Pro Asp Ile Ser Pro Ala Ser Phe His Arg Leu Asp His  
80 85 90

Leu Val Glu Ile Asp Phe Arg Cys Asn Cys Val Pro Ile Pro Leu  
95 100 105

Gly Ser Lys Asn Asn Met Cys Ile Lys Arg Leu Gln Ile Lys Pro  
110 115 120

Arg Ser Phe Ser Gly Leu Thr Tyr Leu Lys Ser Leu Tyr Leu Asp  
125 130 135

Gly Asn Gln Leu Leu Glu Ile Pro Gln Gly Leu Pro Pro Ser Leu  
140 145 150

Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile Phe Ser Ile Arg Lys  
155 160 165

Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile Leu Tyr Leu Gly  
170 175 180

Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser Tyr Ser Ile  
185 190 195

Glu Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val Leu Ser  
200 205 210

Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro Ser  
215 220 225

Thr Leu Thr Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile  
230 235 240

Gln Glu Asp Asp Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp  
245 250 255

protein = 496



Leu Ser Gly Asn Cys Pro Arg Cys Tyr Asn Ala Pro Phe Pro Cys  
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 Ala Pro Cys Lys Asn Asn Ser Pro Leu Gln Ile Pro Val Asn Ala  
 275 280 285  
 Phe Asp Ala Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn  
 290 295 300  
 Ser Leu Gln His Val Pro Pro Arg Trp Phe Lys Asn Ile Asn Lys  
 305 310 315  
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 320 325 330  
 Gly Asp Ala Lys Phe Leu His Phe Leu Pro Ser Leu Ile Gln Leu  
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 Asp Leu Ser Phe Asn Phe Glu Leu Gln Val Tyr Arg Ala Ser Met  
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 Asn Leu Ser Gln Ala Phe Ser Ser Leu Lys Ser Leu Lys Ile Leu  
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 Arg Ile Arg Gly Tyr Val Phe Lys Glu Leu Lys Ser Phe Asn Leu  
 380 385 390  
 Ser Pro Leu His Asn Leu Gln Asn Leu Glu Val Leu Asp Leu Gly  
 395 400 405  
 Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met Phe Lys Gln Phe  
 410 415 420  
 Lys Arg Leu Lys Val Ile Asp Leu Ser Val Asn Lys Ile Ser Pro  
 425 430 435  
 Ser Gly Asp Ser Ser Glu Val Gly Phe Cys Ser Asn Ala Arg Thr  
 440 445 450  
 Ser Val Glu Ser Tyr Glu Pro Gln Val Leu Glu Gln Leu His Tyr  
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 Phe Arg Tyr Asp Lys Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys  
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 Glu Ala Ser Phe Met Ser Val Asn Glu Ser Cys Tyr Lys Tyr Gly  
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 Gln Thr Leu Asp Leu Ser Lys Asn Ser Ile Phe Phe Val Lys Ser  
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 Ser Asp Phe Gln His Leu Ser Phe Leu Lys Cys Leu Asn Leu Ser  
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 Gly Asn Leu Ile Ser Gln Thr Leu Asn Gly Ser Glu Phe Gln Pro  
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Leu Asp Ile Ser Ser Asn Ser His Tyr Phe Gln Ser Glu Gly Ile		
575	580	585
Thr His Met Leu Asn Phe Thr Lys Asn Leu Lys Val Leu Gln Lys		
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Leu Met Met Asn Asp Asn Asp Ile Ser Ser Ser Thr Ser Arg Thr		
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Met Glu Ser Glu Ser Leu Arg Thr Leu Glu Phe Arg Gly Asn His		
620	625	630
Leu Asp Val Leu Trp Arg Glu Gly Asp Asn Arg Tyr Leu Gln Leu		
635	640	645
Phe Lys Asn Leu Leu Lys Leu Glu Glu Leu Asp Ile Ser Lys Asn		
650	655	660
Ser Leu Ser Phe Leu Pro Ser Gly Val Phe Asp Gly Met Pro Pro		
665	670	675
Asn Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys Ser Phe		
680	685	690
Ser Trp Lys Lys Leu Gln Cys Leu Lys Asn Leu Glu Thr Leu Asp		
695	700	705
Leu Ser His Asn Gln Leu Thr Thr Val Pro Glu Arg Leu Ser Asn		
710	715	720
Cys Ser Arg Ser Leu Lys Asn Leu Ile Leu Lys Asn Asn Gln Ile		
725	730	735
Arg Ser Leu Thr Lys Tyr Phe Leu Gln Asp Ala Phe Gln Leu Arg		
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Tyr Leu Asp Leu Ser Ser Asn Lys Ile Gln Met Ile Gln Lys Thr		
755	760	765
Ser Phe Pro Glu Asn Val Leu Asn Asn Leu Lys Met Leu Leu Leu		
770	775	780
His His Asn Arg Phe Leu Cys Thr Cys Asp Ala Val Trp Phe Val		
785	790	795
Trp Trp Val Asn His Thr Glu Val Thr Ile Pro Tyr Leu Ala Thr		
800	805	810
Asp Val Thr Cys Val Gly Pro Gly Ala His Lys Gly Gln Ser Val		
815	820	825
Ile Ser Leu Asp Leu Tyr Thr Cys Glu Leu Asp Leu Thr Asn Leu		
830	835	840

Ile Leu Phe Ser Leu Ser Ile Ser Val Ser Leu Phe Leu Met Val  
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 Met Met Thr Ala Ser His Leu Tyr Phe Trp Asp Val Trp Tyr Ile  
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 Tyr His Phe Cys Lys Ala Lys Ile Lys Gly Tyr Gln Arg Leu Ile  
 875 880 885  
 Ser Pro Asp Cys Cys Tyr Asp Ala Phe Ile Val Tyr Asp Thr Lys  
 890 895 900  
 Asp Pro Ala Val Thr Glu Trp Val Leu Ala Glu Leu Val Ala Lys  
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 Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu Ser Gln  
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 Tyr Ala Lys Thr Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His  
 965 970 975  
 Gln Arg Leu Met Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe  
 980 985 990  
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 995 1000 1005  
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<210> 497

<211> 4199

<212> DNA

<213> Homo sapiens

<400> 497

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gaagctatcc ttgtgatgag aaaaagcaaa atgactcagt tattgcagag 200

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tcaaataattt ggatttgaca aacaatagac tagactttga taatgctagt 1700

Top200: 1302400



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 <211> 1041  
 <212> PRT  
 <213> Homo sapiens

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 Ser Arg Ser Tyr Pro Cys Asp Glu Lys Lys Gln Asn Asp Ser Val  
 35 40 45  
 Ile Ala Glu Cys Ser Asn Arg Arg Leu Gln Glu Val Pro Gln Thr

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Val Gly Lys Tyr	Val Thr Glu Leu Asp	Leu Ser Asp Asn Phe Ile
65	70	75
Thr His Ile Thr	Asn Glu Ser Phe Gln Gly	Leu Gln Asn Leu Thr
80	85	90
Lys Ile Asn Leu	Asn His Asn Pro Asn Val	Gln His Gln Asn Gly
95	100	105
Asn Pro Gly Ile	Gln Ser Asn Gly Leu Asn	Ile Thr Asp Gly Ala
110	115	120
Phe Leu Asn Leu	Lys Asn Leu Arg Glu Leu	Leu Leu Glu Asp Asn
125	130	135
Gln Leu Pro Gln	Ile Pro Ser Gly Leu Pro	Glu Ser Leu Thr Glu
140	145	150
Leu Ser Leu Ile	Gln Asn Asn Ile Tyr Asn	Ile Thr Lys Glu Gly
155	160	165
Ile Ser Arg Leu	Ile Asn Leu Lys Asn Leu	Tyr Leu Ala Trp Asn
170	175	180
Cys Tyr Phe Asn	Lys Val Cys Glu Lys Thr	Asn Ile Glu Asp Gly
185	190	195
Val Phe Glu Thr	Leu Thr Asn Leu Glu Leu	Leu Ser Leu Ser Phe
200	205	210
Asn Ser Leu Ser	His Val Pro Pro Lys Leu	Pro Ser Ser Leu Arg
215	220	225
Lys Leu Phe Leu	Ser Asn Thr Gln Ile Lys	Tyr Ile Ser Glu Glu
230	235	240
Asp Phe Lys Gly	Leu Ile Asn Leu Thr Leu	Leu Asp Leu Ser Gly
245	250	255
Asn Cys Pro Arg	Cys Phe Asn Ala Pro Phe	Pro Cys Val Pro Cys
260	265	270
Asp Gly Gly Ala	Ser Ile Asn Ile Asp Arg	Phe Ala Phe Gln Asn
275	280	285
Leu Thr Gln Leu	Arg Tyr Leu Asn Leu Ser	Ser Thr Ser Leu Arg
290	295	300
Lys Ile Asn Ala	Ala Trp Phe Lys Asn Met	Pro His Leu Lys Val
305	310	315
Leu Asp Leu Glu	Phe Asn Tyr Leu Val Gly	Glu Ile Val Ser Gly
320	325	330
Ala Phe Leu Thr	Met Leu Pro Arg Leu Glu	Ile Leu Asp Leu Ser
335	340	345

Phe Asn Tyr Ile Lys Gly Ser Tyr Pro Gln His Ile Asn Ile Ser  
 350 355 360  
 Arg Asn Phe Ser Lys Leu Leu Ser Leu Arg Ala Leu His Leu Arg  
 365 370 375  
 Gly Tyr Val Phe Gln Glu Leu Arg Glu Asp Asp Phe Gln Pro Leu  
 380 385 390  
 Met Gln Leu Pro Asn Leu Ser Thr Ile Asn Leu Gly Ile Asn Phe  
 395 400 405  
 Ile Lys Gln Ile Asp Phe Lys Leu Phe Gln Asn Phe Ser Asn Leu  
 410 415 420  
 Glu Ile Ile Tyr Leu Ser Glu Asn Arg Ile Ser Pro Leu Val Lys  
 425 430 435  
 Asp Thr Arg Gln Ser Tyr Ala Asn Ser Ser Ser Phe Gln Arg His  
 440 445 450  
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 455 460 465  
 Asn Phe Tyr His Phe Thr Arg Pro Leu Ile Lys Pro Gln Cys Ala  
 470 475 480  
 Ala Tyr Gly Lys Ala Leu Asp Leu Ser Leu Asn Ser Ile Phe Phe  
 485 490 495  
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 530 535 540  
 Arg Leu Asp Phe Asp Asn Ala Ser Ala Leu Thr Glu Leu Ser Asp  
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 Leu Glu Val Leu Asp Leu Ser Tyr Asn Ser His Tyr Phe Arg Ile  
 560 565 570  
 Ala Gly Val Thr His His Leu Glu Phe Ile Gln Asn Phe Thr Asn  
 575 580 585  
 Leu Lys Val Leu Asn Leu Ser His Asn Asn Ile Tyr Thr Leu Thr  
 590 595 600  
 Asp Lys Tyr Asn Leu Glu Ser Lys Ser Leu Val Glu Leu Val Phe  
 605 610 615  
 Ser Gly Asn Arg Leu Asp Ile Leu Trp Asn Asp Asp Asp Asn Arg  
 620 625 630  
 Tyr Ile Ser Ile Phe Lys Gly Leu Lys Asn Leu Thr Arg Leu Asp



635	640	645
Leu Ser Leu Asn Arg Leu Lys His Ile	Pro Asn Glu Ala Phe Leu	
650	655	660
Asn Leu Pro Ala Ser Leu Thr Glu Leu	His Ile Asn Asp Asn Met	
665	670	675
Leu Lys Phe Phe Asn Trp Thr Leu Leu	Gln Gln Phe Pro Arg Leu	
680	685	690
Glu Leu Leu Asp Leu Arg Gly Asn Lys	Leu Leu Phe Leu Thr Asp	
695	700	705
Ser Leu Ser Asp Phe Thr Ser Ser Leu	Arg Thr Leu Leu Leu Ser	
710	715	720
His Asn Arg Ile Ser His Leu Pro Ser	Gly Phe Leu Ser Glu Val	
725	730	735
Ser Ser Leu Lys His Leu Asp Leu Ser	Ser Asn Leu Leu Lys Thr	
740	745	750
Ile Asn Lys Ser Ala Leu Glu Thr Lys	Thr Thr Thr Lys Leu Ser	
755	760	765
Met Leu Glu Leu His Gly Asn Pro Phe	Glu Cys Thr Cys Asp Ile	
770	775	780
Gly Asp Phe Arg Arg Trp Met Asp Glu	His Leu Asn Val Lys Ile	
785	790	795
Pro Arg Leu Val Asp Val Ile Cys Ala	Ser Pro Gly Asp Gln Arg	
800	805	810
Gly Lys Ser Ile Val Ser Leu Glu Leu	Thr Thr Cys Val Ser Asp	
815	820	825
Val Thr Ala Val Ile Leu Phe Phe Phe	Thr Phe Phe Ile Thr Thr	
830	835	840
Met Val Met Leu Ala Ala Leu Ala His	His Leu Phe Tyr Trp Asp	
845	850	855
Val Trp Phe Ile Tyr Asn Val Cys Leu	Ala Lys Val Lys Gly Tyr	
860	865	870
Arg Ser Leu Ser Thr Ser Gln Thr Phe	Tyr Asp Ala Tyr Ile Ser	
875	880	885
Tyr Asp Thr Lys Asp Ala Ser Val Thr	Asp Trp Val Ile Asn Glu	
890	895	900
Leu Arg Tyr His Leu Glu Glu Ser Arg	Asp Lys Asn Val Leu Leu	
905	910	915
Cys Leu Glu Glu Arg Asp Trp Asp Pro	Gly Leu Ala Ile Ile Asp	
920	925	930

Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val  
 935 940 945  
 Leu Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe  
 950 955 960  
 Tyr Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile  
 965 970 975  
 Ile Phe Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu  
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 Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro  
 995 1000 1005  
 Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn  
 1010 1015 1020  
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 <223> Synthetic oligonucleotide probe

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<400> 500  
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<210> 501  
 <211> 45  
 <212> DNA  
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<220>  
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<400> 501  
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<210> 502

<211> 21  
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<223> Synthetic oligonucleotide probe

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gccgagacaa aaacgttctc c 21

<210> 503  
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<400> 503  
catccatggt ctcattcatt agcc 24

<210> 504  
<211> 46  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 504  
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<210> 505  
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<211> 273  
<212> PRT  
<213> Homo sapiens

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 35 40 45  
 Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg  
 50 55 60  
 Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg  
 65 70 75  
 Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro  
 80 85 90  
 Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala  
 95 100 105  
 Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro  
 110 115 120  
 Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln  
 125 130 135  
 Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln  
 140 145 150  
 Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu  
 155 160 165  
 Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly  
 170 175 180  
 Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala  
 185 190 195  
 Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu  
 200 205 210  
 Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala  
 215 220 225  
 Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu  
 230 235 240  
 Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu  
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 Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys  
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 Lys Asp Ser

<210> 507  
 <211> 1700  
 <212> DNA  
 <213> Homo sapiens

<400> 507

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<210> 508  
 <211> 273  
 <212> PRT  
 <213> Homo sapiens

<400> 508  
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Ala Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val  
 20 25 30

Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val  
 35 40 45

Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg  
 50 55 60

Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg  
 65 70 75

Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro  
 80 85 90

Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala  
 95 100 105

Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro  
 110 115 120

Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln  
 125 130 135

Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln  
 140 145 150

Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu  
 155 160 165

Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly  
 170 175 180

Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala  
 185 190 195

Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu  
 200 205 210

FOOTNOTES: 1802

Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala  
 215 220 225  
 Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu  
 230 235 240  
 Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu  
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 Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys  
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 Lys Asp Ser

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 <211> 1538  
 <212> DNA  
 <213> Homo sapiens

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<210> 510

<211> 273

<212> PRT

<213> Homo sapiens

<400> 510

Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu  
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Ala Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val  
20 25 30

Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val  
35 40 45

Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg  
50 55 60

Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg  
65 70 75

Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro  
80 85 90

Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala  
95 100 105

Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro  
110 115 120

Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln  
125 130 135

Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln



<400> 513  
ggtgacactt gccagtcaga tgtggatgaa tgcagtgcta ggaggg 46

<210> 514  
<211> 2690  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 2039-2065  
<223> unknown base

<400> 514  
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ccgacgtgat tccctgggac ggtccgtttc ctgccgtcag ctgccggccg 150  
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<210> 515  
<211> 364  
<212> PRT  
<213> Homo sapiens

<400> 515

Met Ser Val Met Val Val Arg Lys Lys Val Thr Arg Lys Trp Glu  
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Lys Leu Pro Gly Arg Asn Thr Phe Cys Cys Asp Gly Arg Val Met  
20 25 30

Met Ala Arg Gln Lys Gly Ile Phe Tyr Leu Thr Leu Phe Leu Ile  
35 40 45

Leu Gly Thr Cys Thr Leu Phe Phe Ala Phe Glu Cys Arg Tyr Leu  
50 55 60

Ala Val Gln Leu Ser Pro Ala Ile Pro Val Phe Ala Ala Met Leu  
65 70 75

Phe Leu Phe Ser Met Ala Thr Leu Leu Arg Thr Ser Phe Ser Asp  
80 85 90

Pro Gly Val Ile Pro Arg Ala Leu Pro Asp Glu Ala Ala Phe Ile  
95 100 105

Glu Met Glu Ile Glu Ala Thr Asn Gly Ala Val Pro Gln Gly Gln  
110 115 120

Arg Pro Pro Pro Arg Ile Lys Asn Phe Gln Ile Asn Asn Gln Ile  
125 130 135

Val Lys Leu Lys Tyr Cys Tyr Thr Cys Lys Ile Phe Arg Pro Pro  
140 145 150

Arg Ala Ser His Cys Ser Ile Cys Asp Asn Cys Val Glu Arg Phe  
155 160 165

Asp His His Cys Pro Trp Val Gly Asn Cys Val Gly Lys Arg Asn  
170 175 180

Tyr Arg Tyr Phe Tyr Leu Phe Ile Leu Ser Leu Ser Leu Leu Thr  
185 190 195

Ile Tyr Val Phe Ala Phe Asn Ile Val Tyr Val Ala Leu Lys Ser  
200 205 210

Leu Lys Ile Gly Phe Leu Glu Thr Leu Lys Glu Thr Pro Gly Thr  
215 220 225

Val Leu Glu Val Leu Ile Cys Phe Phe Thr Leu Trp Ser Val Val

FOOT=1802FOOT

230	235	240
Gly Leu Thr Gly Phe His Thr Phe Leu Val Ala Leu Asn Gln Thr		
245	250	255
Thr Asn Glu Asp Ile Lys Gly Ser Trp Thr Gly Lys Asn Arg Val		
260	265	270
Gln Asn Pro Tyr Ser His Gly Asn Ile Val Lys Asn Cys Cys Glu		
275	280	285
Val Leu Cys Gly Pro Leu Pro Pro Ser Val Leu Asp Arg Arg Gly		
290	295	300
Ile Leu Pro Leu Glu Glu Ser Gly Ser Arg Pro Pro Ser Thr Gln		
305	310	315
Glu Thr Ser Ser Ser Leu Leu Pro Gln Ser Pro Ala Pro Thr Glu		
320	325	330
His Leu Asn Ser Asn Glu Met Pro Glu Asp Ser Ser Thr Pro Glu		
335	340	345
Glu Met Pro Pro Pro Glu Pro Pro Glu Pro Pro Gln Glu Ala Ala		
350	355	360
Glu Ala Glu Lys		

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 <213> Homo sapiens  
 <220>  
 <221> unsure  
 <222> 36, 38, 88, 118, 135, 193, 213, 222  
 <223> unknown base

<400> 516  
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 cccctgggtg gggaattgtg ttggaaagag gaactaccgc tanttctacc 200  
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 atcgt 255

<210> 517  
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 <213> Artificial Sequence  
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<223> Synthetic oligonucleotide probe

<400> 517

caacgtgatt tcaaagctgg gctc 24

<210> 518

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 518

gcctcgatc aagaatttcc 20

<210> 519

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

agtgaagtc gacctccc 18

<210> 520

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 520

ctcacctgaa atctctcata gccc 24

<210> 521

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 521

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<210> 522

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 522

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 aaaaatgcac aattctatct cttgggcaat cttcacggg ctggtgctc 200  
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aattcaatca gtccatagag acgaacagaa tgagaccttc cggcccaagc 1600  
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<210> 523  
 <211> 344  
 <212> PRT  
 <213> Homo sapiens

<400> 523

Met Lys Thr Ile Gln Pro Lys Met His Asn Ser Ile Ser Trp Ala  
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Ile Phe Thr Gly Leu Ala Ala Leu Cys Leu Phe Gln Gly Val Pro  
 20 25 30

Val Arg Ser Gly Asp Ala Thr Phe Pro Lys Ala Met Asp Asn Val  
 35 40 45

Thr Val Arg Gln Gly Glu Ser Ala Thr Leu Arg Cys Thr Ile Asp  
 50 55 60

Asn Arg Val Thr Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu  
 65 70 75

Tyr Ala Gly Asn Asp Lys Trp Cys Leu Asp Pro Arg Val Val Leu  
 80 85 90

Leu Ser Asn Thr Gln Thr Gln Tyr Ser Ile Glu Ile Gln Asn Val  
 95 100 105

Asp Val Tyr Asp Glu Gly Pro Tyr Thr Cys Ser Val Gln Thr Asp  
 110 115 120

Asn His Pro Lys Thr Ser Arg Val His Leu Ile Val Gln Val Ser  
 125 130 135

Pro Lys Ile Val Glu Ile Ser Ser Asp Ile Ser Ile Asn Glu Gly  
 140 145 150

Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr Gly Arg Pro Glu Pro  
 155 160 165

Thr Val Thr Trp Arg His Ile Ser Pro Lys Ala Val Gly Phe Val  
 170 175 180

Ser Glu Asp Glu Tyr Leu Glu Ile Gln Gly Ile Thr Arg Glu Gln  
 185 190 195

Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp Val Ala Ala Pro  
 200 205 210

Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro Tyr Ile  
 215 220 225

Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly Thr

TEB02T001

230	235	240
Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln Trp		
245	250	255
Tyr Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys Gly Val Lys		
260	265	270
Val Glu Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe Asn Val		
275	280	285
Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys		
290	295	300
Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala		
305	310	315
Val Ser Glu Val Ser Asn Gly Thr Ser Arg Arg Ala Gly Cys Val		
320	325	330
Trp Leu Leu Pro Leu Leu Val Leu His Leu Leu Leu Lys Phe		
335	340	

<210> 524  
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 <212> DNA  
 <213> Homo sapiens  
 <400> 524

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 tccggcaggg ggagagcgcc accctcaggt gcactattga caaccgggtc 200  
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TOP201-18047001

230	235	240
Ile Arg Cys Glu Gly Ala Gly Val Pro	Pro Pro Ala Phe Glu Trp	
245	250	255
Tyr Lys Gly Glu Lys Lys Leu Phe Asn	Gly Gln Gln Gly Ile Ile	
260	265	270
Ile Gln Asn Phe Ser Thr Arg Ser Ile	Leu Thr Val Thr Asn Val	
275	280	285
Thr Gln Glu His Phe Gly Asn Tyr Thr	Cys Val Ala Ala Asn Lys	
290	295	300
Leu Gly Thr Thr Asn Ala Ser Leu Pro	Leu Asn Pro Pro Ser Thr	
305	310	315
Ala Gln Tyr Gly Ile Thr Gly Ser Ala	Asp Val Leu Phe Ser Cys	
320	325	330
Trp Tyr Leu Val Leu Thr Leu Ser Ser	Phe Thr Ser Ile Phe Tyr	
335	340	345
Leu Lys Asn Ala Ile Leu Gln		
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<210> 613  
 <211> 1797  
 <212> DNA  
 <213> Homo Sapien

<400> 613  
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 aaataagaaa attctcaagg aggacgagct cttgagttag acccaacaag 150  
 ctgcttttca ccaaattgca atggagcctt tcgaaatcaa tgttccaaag 200  
 cccaagagga gaaatggggt gaacttctcc ctagctgtgg tggatcatcta 250  
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 atctgcaggc gcggctccgg gtcttgaga tgtatttctt caatgacact 350  
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 cccaggtctt caaggtcaca agggggccat gggcatgcct ggtgcccctg 600  
 gccgcgggg accacctgct gagaaggag ccaagggggc tatgggacga 650

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ctggcacccc aggaccccaa ggagagaagg gcagcaaagg cgatgggggt 800  
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acctggactg caggggtgttc cgggccctcc tgggtgcagtg ggacaccag 1050  
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caggccctgc aggtgtgaag ggagaacagg ggagcccagg gctggcaggt 1250  
cccaagggag cccctggaca agctggccag aaggagagacc agggagtga 1300  
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gaagtttact acagtggtag ctgggggaca atttgcatg acgagtggca 1450  
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<210> 614  
<211> 520  
<212> PRT  
<213> Homo Sapien

<400> 614  
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Thr Gln Gln Ala Ala Phe His Gln Ile Ala Met Glu Pro Phe Glu  
20 25 30



FOH20T-1802T00T

Ile	Asn	Val	Pro	Lys	Pro	Lys	Arg	Arg	Asn	Gly	Val	Asn	Phe	Ser	35	40	45
Leu	Ala	Val	Val	Val	Ile	Tyr	Leu	Ile	Leu	Leu	Thr	Ala	Gly	Ala	50	55	60
Gly	Leu	Leu	Val	Val	Gln	Val	Leu	Asn	Leu	Gln	Ala	Arg	Leu	Arg	65	70	75
Val	Leu	Glu	Met	Tyr	Phe	Leu	Asn	Asp	Thr	Leu	Ala	Ala	Glu	Asp	80	85	90
Ser	Pro	Ser	Phe	Ser	Leu	Leu	Gln	Ser	Ala	His	Pro	Gly	Glu	His	95	100	105
Leu	Ala	Gln	Gly	Ala	Ser	Arg	Leu	Gln	Val	Leu	Gln	Ala	Gln	Leu	110	115	120
Thr	Trp	Val	Arg	Val	Ser	His	Glu	His	Leu	Leu	Gln	Arg	Val	Asp	125	130	135
Asn	Phe	Thr	Gln	Asn	Pro	Gly	Met	Phe	Arg	Ile	Lys	Gly	Glu	Gln	140	145	150
Gly	Ala	Pro	Gly	Leu	Gln	Gly	His	Lys	Gly	Ala	Met	Gly	Met	Pro	155	160	165
Gly	Ala	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Ala	Glu	Lys	Gly	Ala	Lys	170	175	180
Gly	Ala	Met	Gly	Arg	Asp	Gly	Ala	Thr	Gly	Pro	Ser	Gly	Pro	Gln	185	190	195
Gly	Pro	Pro	Gly	Val	Lys	Gly	Glu	Ala	Gly	Leu	Gln	Gly	Pro	Gln	200	205	210
Gly	Ala	Pro	Gly	Lys	Gln	Gly	Ala	Thr	Gly	Thr	Pro	Gly	Pro	Gln	215	220	225
Gly	Glu	Lys	Gly	Ser	Lys	Gly	Asp	Gly	Gly	Leu	Ile	Gly	Pro	Lys	230	235	240
Gly	Glu	Thr	Gly	Thr	Lys	Gly	Glu	Lys	Gly	Asp	Leu	Gly	Leu	Pro	245	250	255
Gly	Ser	Lys	Gly	Asp	Arg	Gly	Met	Lys	Gly	Asp	Ala	Gly	Val	Met	260	265	270
Gly	Pro	Pro	Gly	Ala	Gln	Gly	Ser	Lys	Gly	Asp	Phe	Gly	Arg	Pro	275	280	285
Gly	Pro	Pro	Gly	Leu	Ala	Gly	Phe	Pro	Gly	Ala	Lys	Gly	Asp	Gln	290	295	300
Gly	Gln	Pro	Gly	Leu	Gln	Gly	Val	Pro	Gly	Pro	Pro	Gly	Ala	Val	305	310	315
Gly	His	Pro	Gly	Ala	Lys	Gly	Glu	Pro	Gly	Ser	Ala	Gly	Ser	Pro			



cctgacacag attgatgtca atgtccagga tcatttctgg gatgggaagg 350  
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<210> 616  
 <211> 98  
 <212> PRT  
 <213> Homo Sapien

<400> 616

Met Lys Leu Met Val Leu Val Phe Thr Ile Gly Leu Thr Leu Leu  
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 Leu Gly Val Gln Ala Met Pro Ala Asn Arg Leu Ser Cys Tyr Arg  
 20 25 30  
 Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val  
 35 40 45  
 Ala Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp His Phe Trp  
 50 55 60  
 Asp Gly Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe Ser Glu  
 65 70 75  
 Leu Leu Cys Cys Pro Lys Asp Val Phe Phe Gly Pro Lys Ile Ser  
 80 85 90  
 Phe Val Ile Pro Cys Asn Asn Gln  
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<210> 617  
 <211> 2558  
 <212> DNA  
 <213> Homo Sapien

<400> 617

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<210> 618

<211> 750

<212> PRT

<213> Homo Sapien

<400> 618

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Arg	Arg	Pro	Arg	Trp	Leu	Cys	Ala	Gly	Ala	Leu	Val	Leu	Ala	Gly
				20					25					30
Gly	Phe	Phe	Leu	Leu	Gly	Phe	Leu	Phe	Gly	Trp	Phe	Ile	Lys	Ser
				35					40					45
Ser	Asn	Glu	Ala	Thr	Asn	Ile	Thr	Pro	Lys	His	Asn	Met	Lys	Ala
				50					55					60
Phe	Leu	Asp	Glu	Leu	Lys	Ala	Glu	Asn	Ile	Lys	Lys	Phe	Leu	His
				65					70					75
Asn	Phe	Thr	Gln	Ile	Pro	His	Leu	Ala	Gly	Thr	Glu	Gln	Asn	Phe
				80					85					90

Gln	Leu	Ala	Lys	Gln	Ile	Gln	Ser	Gln	Trp	Lys	Glu	Phe	Gly	Leu	
				95					100					105	
Asp	Ser	Val	Glu	Leu	Ala	His	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro	
				110					115					120	
Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile	Ser	Ile	Ile	Asn	Glu	Asp	Gly	
				125					130					135	
Asn	Glu	Ile	Phe	Asn	Thr	Ser	Leu	Phe	Glu	Pro	Pro	Pro	Pro	Gly	
				140					145					150	
Tyr	Glu	Asn	Val	Ser	Asp	Ile	Val	Pro	Pro	Phe	Ser	Ala	Phe	Ser	
				155					160					165	
Pro	Gln	Gly	Met	Pro	Glu	Gly	Asp	Leu	Val	Tyr	Val	Asn	Tyr	Ala	
				170					175					180	
Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg	Asp	Met	Lys	Ile	Asn	
				185					190					195	
Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val	Phe	Arg	
				200					205					210	
Gly	Asn	Lys	Val	Lys	Asn	Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly	Val	
				215					220					225	
Ile	Leu	Tyr	Ser	Asp	Pro	Ala	Asp	Tyr	Phe	Ala	Pro	Gly	Val	Lys	
				230					235					240	
Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu	Pro	Gly	Gly	Gly	Val	Gln	Arg	
				245					250					255	
Gly	Asn	Ile	Leu	Asn	Leu	Asn	Gly	Ala	Gly	Asp	Pro	Leu	Thr	Pro	
				260					265					270	
Gly	Tyr	Pro	Ala	Asn	Glu	Tyr	Ala	Tyr	Arg	Arg	Gly	Ile	Ala	Glu	
				275					280					285	
Ala	Val	Gly	Leu	Pro	Ser	Ile	Pro	Val	His	Pro	Ile	Gly	Tyr	Tyr	
				290					295					300	
Asp	Ala	Gln	Lys	Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro	Pro	
				305					310					315	
Asp	Ser	Ser	Trp	Arg	Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly	
				320					325					330	
Pro	Gly	Phe	Thr	Gly	Asn	Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His	
				335					340					345	
Ile	His	Ser	Thr	Asn	Glu	Val	Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly	
				350					355					360	
Thr	Leu	Arg	Gly	Ala	Val	Glu	Pro	Asp	Arg	Tyr	Val	Ile	Leu	Gly	
				365					370					375	
Gly	His	Arg	Asp	Ser	Trp	Val	Phe	Gly	Gly	Ile	Asp	Pro	Gln	Ser	

10017084-102404

380	385	390
Gly Ala Ala Val Val His Glu Ile Val Arg Ser Phe Gly Thr Leu		
395	400	405
Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile Leu Phe Ala Ser		
410	415	420
Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr Glu Trp Ala		
425	430	435
Glu Glu Asn Ser Arg Leu Leu Gln Glu Arg Gly Val Ala Tyr Ile		
440	445	450
Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val Asp		
455	460	465
Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu		
470	475	480
Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu		
485	490	495
Ser Trp Thr Lys Lys Ser Pro Ser Pro Glu Phe Ser Gly Met Pro		
500	505	510
Arg Ile Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe Phe		
515	520	525
Gln Arg Leu Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn		
530	535	540
Trp Glu Thr Asn Lys Phe Ser Gly Tyr Pro Leu Tyr His Ser Val		
545	550	555
Tyr Glu Thr Tyr Glu Leu Val Glu Lys Phe Tyr Asp Pro Met Phe		
560	565	570
Lys Tyr His Leu Thr Val Ala Gln Val Arg Gly Gly Met Val Phe		
575	580	585
Glu Leu Ala Asn Ser Ile Val Leu Pro Phe Asp Cys Arg Asp Tyr		
590	595	600
Ala Val Val Leu Arg Lys Tyr Ala Asp Lys Ile Tyr Ser Ile Ser		
605	610	615
Met Lys His Pro Gln Glu Met Lys Thr Tyr Ser Val Ser Phe Asp		
620	625	630
Ser Leu Phe Ser Ala Val Lys Asn Phe Thr Glu Ile Ala Ser Lys		
635	640	645
Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser Asn Pro Ile Val		
650	655	660
Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu Arg Ala Phe		
665	670	675

Ile	Asp	Pro	Leu	Gly	Leu	Pro	Asp	Arg	Pro	Phe	Tyr	Arg	His	Val
				680					685					690
Ile	Tyr	Ala	Pro	Ser	Ser	His	Asn	Lys	Tyr	Ala	Gly	Glu	Ser	Phe
				695					700					705
Pro	Gly	Ile	Tyr	Asp	Ala	Leu	Phe	Asp	Ile	Glu	Ser	Lys	Val	Asp
				710					715					720
Pro	Ser	Lys	Ala	Trp	Gly	Glu	Val	Lys	Arg	Gln	Ile	Tyr	Val	Ala
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Ala	Phe	Thr	Val	Gln	Ala	Ala	Ala	Glu	Thr	Leu	Ser	Glu	Val	Ala
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<210> 621  
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<210> 624  
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<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide probe

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FOOTNOTES